## U.S. DEPARTMENT OF COMMERCE Petent and Trademark Office **SEARCH REQUEST FORM** Attain Poper #11 Requestor's Serial Brown Loen 09/715,249 Name: Number: Phone: 605-1197 Art Unit: \_\_\_\_ 1636 MATLBOX: 11 E12 OFFICE: Search Topic: Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s). Plane seven the commercial movements 2034 SEWID NO. 1. Edward Hart Technical Info Specialist STIC / Biotech CMI 12C14 Tel: 305-9203 STAFF USE ONLY Search Site Terminal time: Elapsed time: Dialog CPU time: Type of Search APS N.A. Sequence Total time: Geninfo Number of Searches: A.A. Sequence SDC DARC/Questel Number of Databases: Structure Bibliographic Other

GenCore version 4.5 Copyright (c) 1993-2000 Compugen Ltd.

Title: Perfect score:

Run on:

OM nucleic - nucleic search, using sw model

Sequence: US-09-715-249-1\_COPY\_1\_2034
2034
1 atgcgaccctccgggacggc.....acatcgttcggaagcgcacg 2034 January 14, 2002, 19:04:15; Search time 2222.52 Seconds (without alignments) 15097.845 Million cell updates/sec

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

.l number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database GenEmbl:\* gb\_pl:\*
gb\_pr:\* gb\_htg:\*
gb\_in:\* gb\_pat:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_htg\_other:\*

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SUMMARIES

444443887654432109887654321177		Result
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## ALIGNMENTS

03-JUL-2001

BASE COUNT	source	FEATURES	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX179384	RESULT 1
/organism="unidentified" /db_xref="taxon:32644" /note="wild type EGFR1" 946 a 1007 c 953 g 727 t	13633	Location/Qualifiers	Patent: WO 0136659-A 1 25-MAY-2001;	Selectable cell surface marker genes	Pippig,S.D. and Veres,G.	1 (bases 1 to 3633)	unclassified.	unidentified	unidentified.		AX179384.1 GI:14599040	AX179384	Sequence 1 from Patent WO0136659.	AX179384 3633 bp DNA PA		
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ggggtgactcc GGGGTGACTCCAAA ggggtgactcc GGGGTGACTCC CcgtaAAGGAA tccatgccttt              CCGTAAAGACCTT TCCATGCCTT TCCATGCAGTC GTGATGAGACT GTGATGAAAACTG HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	atoggootottoatgogaaggogooacatogttoggaa 	ccgtccatcgccactgggatggtgggggccctcctct 	tgoactacggatgcactgggccaggtcttgaaggctg 	aacaccctggtctggaagtacgcagacgccggccatgt 	CCACTACATTGACGGCCCCCACTGCGTCAAGACCTGCC 	goctcaggocatgaacatcacotgoacaggacgggao 	gggtgagccaagggagtttgtggagaactctgagtgcat 	cgtctcttgccggaatgtcagccgaggcagggaatgcgt 	ccaggtctgccatgccttgtgctcccccgagggctgct 	Ctccggtcagaaaccaaaattataagcaacagaggtga 	ttcaggaaacaaaaatttgtgctatgcaaatacaataaa 	gaacataacatccttgggattacgctccctcaaggagat 	agaaatcatacgcggcaggaccaagcaacatggtcagtt 	gtttttgctgattcaggcttggcctgaaaacaggacgga 	tactcctcctctggatccacaggaactggatattctgaa 	Ctccatcagtggcgatctccacatcctgccggtggcatt 	TGAATTTAAAGACTCACTCTCCATAAATGCTACGAATAT
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Db 247 GCCAGTOGGAGCTGCAGAAAAAACCCTCACGACTACAACTCCCAGGACTACACACGCCCAGGACTACACACGCCAGGACTACACACGCCCAGGACTACACACGCCCAGGACTACACACGCCCAGGACTACACACCTCCAGGCCCCCAGGACTACACACCTCCACGCCCCAGGACTACACACCTCCACGCCCCCAGTACACCTCCACGCCCCAGCACTCCACACCTCCACGCCCCAGCACTCCACACCTCCACGCCCCCAGCACTCCACACCTCCACCGCCCCACCACCCCCCCC	AR086089 5532 bp DNA  ION Sequence 3 from patent US 598553.  AR086089.1 GI:10012855  S UNKnown. ISM Unclassified.  CE 1 (bases 1 to 5532)
1207 TICKCKARKCICCICCICTORGACCAKARATIGSATATIC INAMARCICIAMARCHATAL 120 ALCAGAGGGGTTTTTGCTGATTCAGGCTTGCCTGAAAACAGGACGGAC	Db 907 ACAGGCCCCGGGAGAGCGACTGCCTGTTCTGCCGCAAATTCTGAAACGCAATTATTAAAACACTTCAAA 1206  Oy 781 aaggacacctgcccccactcatgctctacaacccaccacgatggatg

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5532)
Ulirich,A., Coussens,L., Hayflick,J.S., Dull,T.J., Gray,A., Tam,A.W., Lee,J., Yarden,Y., Libermann,T.A., Schlessinger,J., Downward,J., Mayes,E.L., Whittle,N., Waterfield,M.D. and
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RSLKEISGDVIISGNINLCYANTINWKLEGTSGWKKIJISKRENSCKATGGVCHA
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GLAKLLGAEEKEYHAEGGKVPIKMMALESILHIYTHGSDVMSYGVTVWELMTFGSKP
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RDPORYLIGGEERMHLPSPTDSNFYRALMDEEDMDVVDADELLIFOGGGFFSSFSTS
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NLQIIRGNWYYENSYALAVLSWYDANKYGLKELPMRNLQEILHGAVRFSNNPALCNVE
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CSGRCRGKSPSDCCHNQCAAGCTGPRESDCLWCRKFBDEATCKDTCPPLMLYNPTYQ
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NICKYTTII DETWINITION
                         /note="EGF extracellular domain"
568. .576
                                                                                                                                   RTPLLSSLSATSNNSTVACIDRNGLQSCPIKEDSFLORYSSDPTGALTEDSIDDTFLP
VPEYINQSVPKRPAGSVONPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNTVQPTC
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/protein_id="CAA25240".1"
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/db_xrefe"taxon:9606"
187. .258
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                                                                                                             VNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGIFKGSTAENAEYLRVAPQS
/note="Asn-linked glycosylation site"
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187. .3819
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Merlino,G.T., Ishii,S., Whang-Peng,J., Knutsen,T., Xu,Y.-H., Clark,A.J.L., Stratton,R.H., Wilson,R.R., Ma,D.-P.P., Roe,B.A., Hunts,J.H., Shimizu,N. and Pastan,I. Structure and localization of genes encoding aberrant and normal epidermal growth factor receptor RNAs from A431 human carcinoma
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                                                                                                                         draft entry and printed copy of this covided by G.Merlino (07-OCT-1985).
Location/Qualifiers
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/gene="EGFR"
/note="EGFR(S) mRNA; G00-120-610"
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                                              /map="7p13-p12"
<1. .>2643
                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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Danielsen,A.J., Schehl Sinclair,C., Pearsail,R.S., Green,P.J.,
Yee,D., Lampland,A.L., Balasubranan,M.S., Crossley,T.D.,
Magnuson,T.R., James,C.D. and Maihle,N.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2864)
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Direct Submission
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                                         /Protein_ld="Aag43240.1"
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extracellular domain of the receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="truncated epidermal growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="7p11.2-p12"
/tissue_type="placenta"
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           LCSPEGCWGPEPRDCVSCRNVSRGRECVDKCNLLEGEPREFVENSEC IQCHPECLPQA
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TYGPGNESLKAMLFCLFKLSSCNQSNDGSVSHQSGSPAAQESCLGWIPSLLPSEFQLG
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2393)
Xu,Y.H., Ishii,S., Clark,A.J., Sullivan,M., Wilson,R.K., Ma,D.P.,
Roe,B.A., Merlino,G.T. and Pastan,I.
Human epidermal growth factor receptor CDNA is homologous to a variety of RNAs overproduced in A431 carcinoma cells
Nature 309 (5971), 806-810 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-MAY-1985) to the EMBL/GenBank/DDBJ databases Data kindly reviewed (28-05-1985) by Merlino G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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AFENLEIIRGRTKCHGQFSLAVVSLNITSLGLRSLKEISGDKGLGSUKHLCYAMTIN
WKKLFGTSGQKTKIISNRGENSCKATGQVCHALCSPEGGWGPEPRDCVSCRNVSRGRE
CVDKCNLLEGEPREFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCV
                                                                                                                                                                                                                                                                                                                                                     /db_xref="SWISS-PROT:P00533"
/translation="ILHCAVRESUNPALCOVESIGWRDIVSSDELSNMSMDFQNHLGS
COKCDPSCPMSCWGAGEENCOKLTKIICAOOCSGRCRGKSPSDCCHNOCAAGCTGPR
CSDCLVCRKERDEATCKDTCPPLMLYNPTTYOMDVNPEGKYSFGATCVKKCPRNYVVT
DHGSCVRACGADSYEMEEDGVRRCKKCEGFERKVCNGIGIGEFKDSLS:NATNIKHFK
NGGGJGCVRACGADSYEMEEDGVRRCKKCEGFERKVCNGIGIGEFKDSLS:NATNIKHFK
                                                                                                       ETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREATSPKANKEILDEAYVM
ASVDNPHVCRLLGICLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKG
MNYLEDRRLVHRDLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMA
                                                                                                                                                                                             KTCPAGVMGENNTLVMKYADAGHVCHLCHPNCTYGCTGPGLEGCPTNGPKIPSIATGM
VGALLLLLVVALGIGLFMRRRHIVRKRTLRRLLQERELVEPLTPSGEAPNQALLRILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAA25282.1"
/db_xref="GI:4378981"
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Paria,B.C., Das,S.K., Andrews,G.K. and Dey,S.K.
Expression of the epidermal growth factor receptor gene is regulated in mouse blastocysts during delayed implantation proc. Natl. Acad. Sci. U.S.A. 90 (1), 55-59 (1993)
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DFGLAKLLGAEEKEYHAEGGKVPIKMMALESILHRIYTHQSDVWSYGVTVWELMTFGS
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EILKTYKEITGELLIQAWPDNWTDLHAFENLEIIRGRTKGHGGFSLAVVGLNITSLGL
RSLKEISDGDVIISGNRNLCYANTINKKKLFGTPNOKTKINNNRAEKDCKAVNHVCNP
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                                                      TTCGGGACACCCAATCAGAAAACCAAAATCATGAACAACAGAGCTGAGAAAGACTGCAAG
                                                                                                                              GTGATCATTTCTGGAAACCGAAATTTGTGCTACGCAAACACACAATAAACTGGAAAAAACTC
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Threadmill n.W., Elev,G.D., Strunk,K.E.,
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Comparative genomic sequence analysis and isolation of human and
                                                                                                                                                        Submitted (07-JUN-2000) Department of Cell Biology, Vanderbilt University, 1161 21st Ave. S. Nashville, TN 37232-2175, USA
                                                                                                                                                                                                                                   Reiter,J.L., Threadgill,D.W., Eley,G.D., Strunk,K.E., Danielsen,A.J., Schehl,C., Pearsall,R.S., Green,P.J., Yee,D., Lampland,A.L., Balasubramaniam,S., Crossley,T.O., Magnuson,T.R.,
                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                              mouse alternative egfr transcripts encoding truncated receptor
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    /gene≈"Egfr"
224. .3856
                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                           /db_xref="taxon:10090"
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LCSSEGCWGPEPRDCVSCONVSRGRECVEKCNILEGEPREFVENSECIOCHECLEON
MNITCUGREGDNCIOCAHYLDGEHCVKTCAGAGHGENNTLWKYADANNWCHLCHANC
TYGCAGFLOCCEWPASGEKIESIATGIWGLLEI IVVVALGILEIGLEWRRHITURKRTLR
RLLQERELVEPLTPSGEAPNQAHLRILKETEFKKIKVLGSGAFGTVYKGLMIPEGEKV
KIPVALKELREATSPRANKEILDEAYVNASVDNEHVCRLLGICLTSTVQLATQLWBYG
CLLDVREHKDNIGSGYLLMWCVQIAKGNWYLDERRLUHRDLAARWYLKFTPGHVKIT
DFGLAKLLGAEEKEYHAEGGKVFIKWAALESILHRIYTHOSDVWSYGTWWELMTFGS
KYDGIFANDISSILEKGREUDPFICTIOVYMIMYKGMIDADEKTTFGELILLEESK
WARDDGRYLVIGGDERHLESFDSNIYYALMDEEDMEDVDADEKTTFGDGFFWSFS
KARDDGRYLVIGGDERHLESFDSNIYYALMDEEDMEDVDADEKTTFGDGFFWSFS
TSRTPLLSSISATSNISTYACIRRIGSCRYKEDAFLQRYSSDPTGAVTEDNINDAFLP
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TIQWRDI VQNYFMSMISMDLQSHPSSCPKCDPSKPNSKGGEERNQKLTK I ICAQQ
CSHRCRGRESPEDCCHNQCARGTTGPRESDCLIVQKKYDDEAYCKDTCPPLMLYNPTTYQ
MDVNPEGKYSEGATCVKKCPRNYVYTDHGSCVRACGPDYEVEEDGIRKCKKCDGPCR
KYCNGI GIGEFKDTLS INATNIKHFKYCTA ISGDLHILPVAFKGDSSTRTPPLDBREL
EILKYVKETIGFLLI QAMPDNWFDLHAFENLE II RGRYKQFGJELAVGLHTTSIGL
RSLKEISDGDVII SGNRNLCYANTINWKKLFGTPNQKTKIMNNRAEKDCKAVNHYCNP
VPEYVNQSVPKRPAGSVQNPVYHNQPLHPAPGRDLHYQNPHSNAVGNPEYLNTAQPTC
LSSGFNSPALWIQKGSHQMSLDNPDYQQDFFPKETKPNGIFKGPTAENAEYLRVAPPS
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/protein_ld="AAG24386.1"
/db_xref="G1:10880776"
/translation="MRPSGTARTTLLVLLTALCAAGGALEEKKYCQGTSNRLTQLGTF
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481 agcatccagtggcgggacatagtcagcagtgactttctcagcaacatgtcgatggacttc 121 ttgggcacttttgaagatcattttctcagcctccagaggatgttcaataactgtgaggtg 180 224 ATGCGACCCTCAGGGACCGCGAGAACCACACTGCTGCTGCTGCTGACCGCGCTCTGCGCC 283 644 CAGGAAATCCTGATTGGTGCTGTGCGATTCAGCAACAACCCCATCCTCTGCAATATGGAT 703 584 ATCCTGTCCAACTATGGGACAAACAGAACTGGGCTTAGGGAACTGCCCCATGCGGAACTTA 643 344 CTGGGCACTTTTGAAGACCACTTTCTGAGCCTGCAGAGGATGTACAACAACTGTGAAGTG 284 GCAGGTGGGGCGTTGGAGGAAAAGAAAGTCTGCCAAGGCACAAGTAACAGGCTCACCCAA 343 1 atgogaccotcoggggacgggggcaggggctcottggcotggctggctggctggctggctctgcccg 60 ACTATCCAGTGGAGGGACATCGTCCAAAACGTCTTTATGAGCAACATGTCAATGGACTTA TTGGAGAACCTGCAGATCATCAGGGGAAATGCTCTTTATGAAAACACCTATGCCTTAGCC ttggaaaacctgcagatcatcagaggaaatatgtactacgaaaattcctatgccttagca 360 ACCATCCAGGAGGTGGCCGGCTATGTCCTCATTGCCCTCAACACCGTGGAGAGAATCCCT accatccaggaggtggctggttatgtcctcattgccctcaacacagtggagcgaattcct 300 gcgagtcgggctctggaggaaaagaaagtttgccaaggcacgagtaacaagctcacgcag 120 0; Mismatches 333; Indels DB 10; Length 5935; 6; Gaps 463 403 1:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-NOV-1991) Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Manning Dr. Chapel Hill, NC 27599-7295, USA
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Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence update by submitter on Nov 30, 1999 this sequence version replaced gi:204000
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M37394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                 /gene="Egfr"
154. .3783
                                                                                                                                                                                                                          /db_xref="taxon:10116"
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Rodentia;
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694 CAGCGCCACCTGACGGGCTGCCCGAAATGTGATCCGAGCTGTCCCAATGGAAGCTGCTGG
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                                                                                                                                                                                                                                                                                          CAGGAAATTCTGATCGGTGCTGTGCGATTTAGCAACAACCCCATCCTCTGCAATATGGAG 633
                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCCTGTCCAACTATGGAACCAACAAAACTGGGCTTAGGGAACTGCCCCATGCGGAACTTA 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtcttatctaactatgatgcaaataaaaccggactgaaggagctgcccatgagaaattta 420
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                                                                                                                                               ACCATCCAGTGGAGGGACATCGTCCAAGATGTCTTTCTGAGCAACATGTCAATGGACGTA 693
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1440	11 gtgataatttcaggaaacaaaaatttgtgctatgcaaatacaataaactggaaaaaactg	13	4d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The mouse waved-2 phenotype results from a point mutation in the EGF receptor tyrosine kinase Genes Dev. 8, 399-413 (1994)
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Luetteke.N.C., Phillips,H.K., Qiu,T.H., Copeland,N.G., Earp,H.S., Jenkins,N.A. and Lee,D.C.
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CSHRCRGRSSDCCHQCAAGCTGPRESDCLVCQKFCDBACKCDTCPLMLYNPTTYQ

CSHRCRGRSSDCCHQCAAGCTGPRESDCLVCQKFCDBACKCDTCPLMLYNPTTYQ

MDVNPEEKKYSFCARCVKKCPRAVVYDDBGSCVGACGCPSLAVVCLMITSLGL

EILKTVKETTGFLLIQAAPDNWTDLHAFENLEI RGFKZHGCPSLAVVCLMITSLGL

EILKTVKETTGFLLIQAAPDNWTDLHAFENLEI RGFKZHCPRESCEJCHPECLPQA

MNITCTGRGDDNCIGCHWYNTOLFARENLEI RGFKZHVENSECJCHPECLPQA

MNITCTGRGDDNCIQCAHY I DGPHCVKTCPAGI MGENNTLVWKY ADANNVCHLCHANC

TYGCAGGPLQGCFWPSGGF HSSIATGI VGGLLFI VVYALGI GLFAWARTH JYKKFTLR

RLLQERELVEPTTPSGBAPNQAHLRI LKETEFKK I KYLGSGAFGTYVKGGMIPECEKV

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/protein_id="AAA17899.1"
/db_xref="GI:458124"
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/db_xref="taxon:10090"
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840	aggacacctgccccccactcatgctctacaaccccacgcacg	781	Ŷ
830	ACTGTCTGGTCTGCCAAAAGTTCCAAGATGAGGCCACATG	771	망
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470	CCAACTATGGGACAAACAGAACT	411	
420	tratotaactargatgcaaataaaaccggactgaaggagctgcccatgagaaattt	361	Ŷ
410	TTGGAGAACCTGCAGATCATCAGGGGAAATGCTCTTTATGAAAACACCTATGCCTTAGCC	351	ръ
360	tggaaaacctgcagatcatcagaggaaatatgtactacgaaaattcctatgccttagc	301	8
350	ACCATCCAGGAGGTGGCCGGCTATGTCCTCATTGCCCTCAACACCGTGGAGAGAGA		Дb
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	GTCCTTGGGAACTTGGAAATTACCTATGTGCAAAGGAATTACGACCTTTCCTTAAAG	Lat	ф
240	tccttgggaatttggaaattacctatgtgcagaggaattatgatctttccttcttaaa	181	Ş
230	CTGGGCACTTTTGAAGACCACTTTCTGAGCCTGCAGAGGATGTACAACAACTGTGAAGTG	171	ДЪ
180	tgggcacttttgaagatcattttctcagcctccagaggatgttcaataactgtgagg	121	Qy

KEYWORDS SOURCE ORGANISM

ACCESSION VERSION DEFINITION

AF124513 2618 bp mrNA ROD 26-JAN-2001 Mus musculus epidermal growth factor receptor (Egfr) mrNA, alternatively spliced, complete cds. AF124513 AF124513.1 GI:5524152

REFERENCE AUTHORS

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 2618)

Reiter J.L., Threadgill, D.W., Eley, G.D., Strunk, K.E.,

Danielsen, A.J., Schehl Sinclair, C., Pearsall, R.S., Green, P.J.,

Yee, D., Lampland, A.L., Balasubramaniam, S., Crossley, T.D.,

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Threadgill, D.W. and
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Comparative genomic sequence analysis and isolation of human and mouse alternative egfr transcripts encoding truncated receptor
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Ave S, Nashville, TN 37232-2175, USA
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/protein_id="AAD44149.1"
/db_xref="G1:5524153"
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215. .2182
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/note="Erbbl; alternatively spliced"
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/db_xref="taxon:10090"
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Direct Submission
Submitted (07-FEB-1996) Jill L. Reiter,
Submitted (07-FEB-1996) Jill L. Reiter,
Blology, Mayo Clinic, 200 First St. SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reiter, J.L. and Maihle, N.J.
A 1.8 kb alternative transcript from the human epidermal growth factor receptor gene encodes a truncated form of the receptor Mucleic Acids Res. 24 (20), 4050-4056 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1593)
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/codon_start=1
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/db_xref="G1:1628550"
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245. .1462
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/tissue_type="placenta"
1. .1456
                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
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                           CAGGAAATCCTGCATGGCGCCGTGCGGTTCAGCAACAACCCTGCCCTGTGCAATGTGGAG
                                                   caggaaatcctgcatggcgcgtgcggttcagcaacaaccctgccctgtgcaacgtggag
                                                                                                                                               gtcttatctaactatgatgcaaataaaaccggactgaaggagctgcccatgagaaattta
                                                                                                                                                                                                                     TIGGAAAACCTGCAGATCATCAGAGGAAATATGTACTACGAAAATTCCTATGCCTTAGCA
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/gene-"EGFR"
/note-"5' splice donor site"
1463. 1569
1463. 1542
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CSGRCRGKSPSDCCHNQCAAGCTGPRESDCLVCRKFRDEATCKDTCPPLMLYNPTTYQ
MDVNPEGKYSFGATCVKKCPRNYVYTDHGSCVRACGADSYEMEEDGVRKCKKCEGPCR
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1298. .1306
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                                        Patent:
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                       growth factor receptor-like gene product and its uses
US 5708156-A 1 13-JAN-1998;
Location/Qualifiers
1. .1868
      /organism="unknown"
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                                                         GTGACAGATCACGGCTCGTGCGTCCGAGCCTGTGGGGCCCGACAGCTATGAGATGGAGGAA
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GACGGCGTCCGCAAGTGTAAGAAGTGCGAAGGGCCCTTGCCGCAAAGTGTGTAACGGAATA

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                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-MAR-1997) Obstetrics & Gynecology, University of Ilihoois at Chicago, 820 S. Wood Street, Chicago, IL 60612, USA please also see Ilekis, J. in RK Miller, HA Thiede (eds): 'Molecular Biology and Cell Regulation of the Placenta.' New York: Plenum, 103-117, 1991.
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Expression of a Truncated Epidermal Grov
Protein (TEGFR) in Ovarian Cancer
Gyn. Onc. 65 (1997) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ilekis, J.V., Stark, B.C. and Scoccia, B. Possible role of variant RNA transcripts in epidermal growth factor receptor expression Mol. Reprod. Dev. 41 (2), 149-156 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1868)
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                                                                                                                                                                                                                                                                                    /organisme"Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
504. 575
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                             /translation="mrpsgtagaallallaalcpasraleekkvcogtskkltqlgtf
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siqmrdinssdeilsnmsmofonhigscokcopscyngscyngeilhgavrytriicaqo
csgrcrgkspsdcchnocaagctgpresdclvcrkfrdeatckdtcpplmlynptyq
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                                                                                                                            /product-"truncated epidermal growth protein precursor" /protein_d="An#53063.1" /db_xref="GI:2051985"
   DILKTVKEITGLS"
                                                                                                                                                                                                       /note="TEGFR; the calculated molecular weight of the nascent protein is approximately 42 kb (includes signal peptide at amino acid positions 1-24); the molecular weight of the mature protein is approximately 80 kD; secreted growth factor receptor"
                  KVCNGIGIGEFKDSLSINATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQEL
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                                                                cccgagggcaaatacagctttggtgccacctgcgtgaagaagtgtccccgtaattatgtg
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360 803 240 683

Search completed: January 14, 2002, 20:13:47 Job time: 4172 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                   N_Geneseq_1101:*

//SIDSZ/gcgdata/geneseq/geneseqn/NA1980.DAT:*

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SUMMARIES
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Result No. 1	; ,	Query Match Length DB 100.0 3633 23	ength 1	- io ;	ID
21	2034 2034	100.0	3633 3818	22 21	AAF85332 AAC61552
ω	2034	100.0	5532	21	AAZ23954
4 1	572.4	77.3	6274	14	AAQ43812
5 1	.425.8	70.1	6207	14	AAQ43813
6 1	207.8	59.4	1868	19	AAV05408
7	992	48.8	1958	22	AAC84211
89	186	48,2	5750	14	AAQ43814
9	431	21.2	5484	22	AAH47973
10	431	21.2	5501	15	AAQ64896
11	431	21.2	5501	17	AAT18532

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	u U	12	
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22	22	22	22	22	22	21	21	11	12	22	21	21	18	21	15	12	20	19	17	20	21	14	22	20	17	21	22	21	18	16	21	17	15	
AA101671	AAI33050	AAI11743	AAI06667	AAI46199	AAI20955	AAC61546	AAC61547	AAQ06828	AAQ12224	AAH42210	AAA89737	AAZ50586	AAT72725	AAA89753	AAT01590	AAQ13363	AAX60313	AAV58734	AAT10059	AAZ31071	AAA14812	AAQ46083	AAH23392	AAX01912	AAT40739	AAA89736	AAF24297	AAZ60815	AAT71253	AAT01585		AAT18533	AAQ64898	
used	Probe #1736 used t	Probe #1676 for ge-	Probe #6658 used t		Probe #10888 for g		_		EGRF-R erbB-3 gene	Nucleotide sequenc	Mouse Her-2/neu cD	DC8scFv-erbB2EC fu	Her2-GM-CSF immuno	Rat HER-2/neu prot		HER-3 epithelial g	E3-16 cDNA clone e	ErbB-3 glycoprotei	erbB-3 cDNA clone	HER-2 nucleic acid	cDNA encoding the	Sequence encoding	Human HER-2/neu pr	Human HER-2/neu on	HER-2/neu oncogene	Human HER-2∕neu co		Nucleotide sequenc	Human HER2 gene.	Her-2/neu (ERBB2/c	Human heregulin 2	Receptor tyrosine	HER4 with alternat	

## ALIGNMENTS

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RESULT
AAF85332
  19-NOV-1999; 99US-0166594.
19-NOV-1999; 99US-0444038.
30-MAR-2000; 2000US-0539248.
                                                                                                                                                                                                                              Epidermal growth factor receptor 1; EGFR1; cell surface marker; protein-tyrosine kinase receptor; PTKR; immunoselection; gene therapy; bone marrow transplant; graft facilitation; immune reconstitution; ss.
                                                                                                                                                                                                                                                                                                                         AAF85332;
                                                                                                                                                                                                                                                                                                                                            AAF85332 standard; DNA; 3633 BP
(NOVS ) NOVARTIS AG.
                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                            Nucleotide sequence of wild type EGFR1.
                                                                                                                                                                                                                                                                                                   23-JUL-2001 (first entry)
                                                                          17-NOV-2000; 2000WO-EP11474
                                                                                                25-MAY-2001.
                                                                                                                      WO200136659-A2
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                                                                                                                                                                          Location/Qualifiers
1..3633
                                                                                                                                         /*tag= a
/transl_except= "(pos: 1618..1620, aa: Asn)"
/product= "EGFR1"
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Query Match
Best Local Similarity
Matches 2034; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying genetically modified mammalian cells for use in e.g. bone marrow transplants, comprises use of mutated protein-tyrosine kinase
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The specification describes a method for diagnosing glioma in a brain cell sample suspected of being cancerous. The method comprises detect the presence of a nucleic acid encoding an epidermal growth factor
                                                   Diagnosing glioma in brain cell sample involves determining the presence of a nucleic acid encoding an epidermal growth factor receptor mutant protein type \Pi .
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atgcgaccctccgggacggccggggcagcgctcctggcgctgctgctgctgcgctctgcccg 246

187

Query Match
Best Local Similarity Matches 2034;

100.0%;

Score 2034; Pred. No. 0; Mismatches

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Conservative

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Sequence 5532 BP; 1472 A; 1484 C; 1337 G; 1239 T;

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01-NOV-1991;
05-MAR-1986;
                                    This invention describes a novel purified nucleic acid (I) (v-erbB related gene) specifically hybridizing to all or part of a MAC117 gene and not hybridizing to nucleic acid encoding an epidermal growth factor receptor. The product of the invention has anticancer and cytostatic activity. Antibodies to the protein encoded by (I) are conjugated to toxins and kill cancer cells expressing (I). Antibodies to the protein encoded by (I) are useful for the treatment of cancer. Fragments of (I) and the MAC117 gene are useful as probes for the detection of human mammary carcinoma or other malignancies resulting from the v-erbB related gene. This sequence encodes a human epidermal growth factor (EGF)
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                                                                                                                                                                                                  Disclosure; Column 19-30; 32pp; English.
                                                                                                                                                                                                                                             Purified nucleic acid useful for detection and treatment
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                           receptor described in the invention.
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/product* "EGF receptor"
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RESULT AAQ43812 AAQ43812 standard; DNA; 6274 BP 4

20-OCT-1993 (first entry)

pRLD1D2D3.ApaL construct.

Epidermal growth factor receptor truncate protein; EGF; growth; binding sites; adsorptive agents; mammallan cell growth abnormality; detection; reproduction; signal transmission; pRLDID2D3ApaL; ds.

Synthetic

Key

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                             ery Match 77.3%;
Best Local Similarity 99.6%;
Matches 1587; Conservative
Sequence 6274 BP; 1506 A; 1610 C; 1664 G; 1493 T; 1 other;
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P-PSDB; AAR38209.
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/note= "codon ARA encodes Ile"
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1440	tgataatttcaggaaacaaaaatttgtgctatgcaaatacaa	1381	Qy
2043	gtcagcctgaacataacatccttgggattacgctccctcaaggagataagtgatggagat	1984	Db
1380	toagcotgaacataacatcottgggattacgctcoctcaaggagataagtgatggaga	1321	Qy
1983	ctagaaatcaracgcggcaggaccaagcatcagtcttctctttgc	1924	Db
1320	agaacctagaaatcatacgcggcaggaccaagcaagcatggtcagttttctcttgcagt	1261	Qy
1923	atcacagggtttttqctgattcaggcttggcctgaaaacaggacggacctccatgccttt	1864	Db
1260	tcacagggtttttgctgattcaggcttggcttgaaaacaggacggac	1201	Qy
1863	ttcacacatactcctcctctggatccacaggaactggatattctgaaaaccgtaaaggaa	1804	Db
1200	tcacacatactcctcctctggatccacaggaactggatattctgaaaaccgtaaagga	1141	γo
1803	aactgcacctccatcagtggcgatctccacatcctgccggtggcatttaggggtgactcc	1744	дb
1140	actgcacctccatcagtggcgatctccacatcctgccggtggcatttaggggtgactc	1081	γQ
1743	ggtattggtgaatttaaagactcoctctccotaaatgctacgaatattaaacacttcaaa	1684	da
1080	gtattggtgaatttaaagactcactctccataaatgctacgaatattaaacacttcaa	1021	γQ
ġ,	9409909t009Caagt9taa9aa9t9c9aa9990ctt9c09caaa9t9t9taac9gaata	1624	Дb
1020	Acggcgtccgcaagtgtaagaagtgcgaagggccttgccgcaaagtgtgtaacggaat	961	Ωy
1623	gtgacagatcacggctcgtgcgtccgaggcctgtgggggccgacagctatgagatggaggaa		фd
960	tgacagatcacggctcgtgcgtccgagcctgtggggccgacagctatgagatggagga	901	Qy
1563	cccgagggcaaatacagctttggtgccacctgcgtgaagaagtgtccccgtaattatgtg	1504	Дb
900	ccgagggcaaatacagctttggtgccacctgcgtgaagaagtgtccccgtaattatgt	841	Ωу
1503	asysacacctyccccactcatyctctacaaccccacctaccagatygatytgaac	1444	фa
840	aggacacctgcccccactcatgctctacaaccccaccacgtaccagatggatg	781	Qy
1443	acaggccccgggagagcgactgcctggtctgccgcaaattccgagacgaagccacgtgc	1384	da
780	gagosococoggagagosacosocococococococococococococococococ		Qy
1383	gggcgctgccgtggcaagtcccccagtgactgctgccacaaccagtgtgctgcaggctgc		Дb
720	gycyctyccytygcaaytcccccagtgactyctgccacaaccagtytyctycagycty	661	Qy
1323	ggtgcaggagaggagactgccagaaactgaccaaaatcatctgtgcccagcagtgctcc		מם
099	gtycagyagagagaactyccayaaactgaccaaaatcatctytycocagcagtyctc	601	Qy
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600	agaaccacctgggcagctgccaaaagtgtgatccaagctgtcccaatgggagctgctg	541	QY
1203	agcatccagtggcgggacatagtcagcagtgactttctcagcaacatgtcgatggacttc		da
540	gcatccagtggcyggacatagtcagcagtgactttctcagcaacatgtcgatggactt	481	Оу
1143	caggaaatcctgcatggcgcgtgcggttcagcaaccaacc	1084	дд
460	aggaaatcctgcatggcgccgtgcggttcagcaacaaccctgccctgtgcaacgtqga	421	Qy
1083	gtcttatctaactatgatgcaaataaaaccggactgaaggagctgcccatgagaaattta	1024	da
420	tottatotaactatgatgcaaataaaaccggactgaaggagctgcccatgagaaattt	361	Qy
1023	ttggaaaacctgcagatcatcagaggaaatatgtactacgaaaattcctatgccttagca	964	מם
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The sequence is that of the pRLD203D4 construct which encodes the epidermal growth factor (EGF) receptor truncate protein in 102D3D4 having EGF binding sites. The protein binds ligands of the EGF receptor without transmitting a signal for the growth and reproduction of a cell. It can be used as an adsorptive agent for any moleties that bind the EGF receptor as the portal of entry to a cell. It competes with the EGF receptor present on the cell surface for the binding of ligands and thereby inhibits the action of the ligands or prevents the entry of viruses into cells. It can also be used as for the EGF receptor itself, such as in the detection of abnormalities in mammalian cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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Ilekis JV;
                       (ILEK/) ILEKIS J V.
                                                    31-MAY-1996;
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/oote= "putative signal peptide"
576..1718
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  1104
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P-PSDB; AAW33737.
                                                                            1044
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                   ggtgcaggagaggagaactgccagaaactgaccaaaatcatctgtgcccagcagtgctcc 660
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                                                                                                                                                                                                                                        EGF receptor related protein (ERRP) encoding cDNA.
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        (USGO ) US DEPT VETERANS AFFAIRS
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888 catcgctgtcgtggcaggtcccccagtgactgctgccacaaccaatgtgctgcgggggtgt 947
                                              661 gggcgctgccgtggcaagtcccccagtgactgctgccacaaccagtgtgctgctgcaggctgc 720
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                                                                                                                                                                                                                              ggtgcaggagaggagactgccagaaactgaccaaaatcatctgtgcccagcagtgctcc
                                                                                                                                                                                                                                                                                                                                                                                                                        cagaaccacctgggcagctgccaaaagtgtgatccaagctgtcccaatgggagctgctgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agcatccagtggcgggacatagtcagcagtgactttctcagcaacatgtcgatggacttc
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Pred. No. 3.1e-274;
0; Mismatches 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1958;
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                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                     Epidermal growth factor receptor truncate protein; EGF; binding sites; adsorptive agents; mammalian cell growth detection; growth; reproduction; signal transmission; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1248
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12-JUN-1990;
                                  12-JUN-1990;
                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                 pRLD3D4 construct.
                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ43814 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1321 gtcagcctgaacataacatccttg 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1081 aactgcacctccatcagtggcgatctccacatcctgccggtggcatttaggggtgactcc 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cctgaagggaagtacagctttggtgccacctgtgtgaagaactgccccgaaactacgtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acaggcccccgggagagcgactgcctggtctgccgcaaattccgagacgaagccacgtgc 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ataacagggtctttgctgattcaggcttggcctgaaaactggactgacctccatgctttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tactgcactgccatcagcggggaccttcacatcctgccagtggcctttaagggggattct 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gatggcatccgcaagtgtaaaaaatgtgatgggccctgtcgcaaagtttgtaatggcata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtgacagatcacggctcgtgcgtccgagcctgtggggccgacagctatgagatggaggaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggcattggtgaatttaaagacscactctccataaatgctacaaacatcaaacacttcaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtgacagatcatggctcatgtgtccgagcctgtgggcctgactactacgaagtggaagaa 1187
90US-0536B96
                                  90US-0536896
                                                                                                                                                                              Location/Qualifiers
1077..1079
                                                                                                                                            /note= "codon ARA encodes Ile"
                                                                                                                                                                                                                                                                     reproduction; signal transmission; ds
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                                                                                                                                                                                                                                                                                        growth abnormality;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of the pRLD3D4 construct which encodes the epidermal growth factor (ESF) receptor truncate protein LD3D4 having ESF binding sites. The protein binds ligands of the ESF receptor without transmitting a signal for the growth and reproduction of a cell. It can be used as an adsorptive agent for any moletles that bind the ESF receptor as the portal of entry to a cell. It competes with the ESF receptor present on the cell surface for the binding of ligands and thereby inhibits the action of the ligands or prevents the entry of viruses into cells. It can also be used as for the EGF receptor itself, such as in the detection of abnormalities in mammalian cell growth. It is also useful for preps novel receptors for efficient detection of ligands and their anti-agonists or agonists. The features table indicate a discrepancy between the LD3D4 protein sequence given in the specification and that which the pRLD3D4 DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local .
                                                                                                                                                                                                                   1059
              1439 tgtttgggacctccggtcagaaaaccaaaattataagcaacagaggtgaaaacagctgca
                                                                                                                                                                                                                                                                                                                            1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1019 taggtattggtgaatttaaagactcactctccataaatgctacgaatattaaacacttca 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5750 BP; 1367 A; 1479 C; 1536 G; 1367 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 9; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New epidermal growth factor receptor truncate proteins - which bind ligands of EGF receptor without transmitting signal for growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      959 aagacggcgtccgcaagtgtaagaagtgcgaagggccttgccgcaaagtgtgtaacggaa 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1990; 90US-0604728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                          cetteacacatactectetggatecacaggaactggatattetgaaaaccgtaaagg 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                        aaaactgcacctccatcagtggcgatctccacatcctgccggtggcatttaggggtgact 1138
                                                                     atgtgataatttcaggaaacaaaatttgtgctatgcaaatacaataaactggaaaaaac
                                                                                                       atgtgataatttcaggaaacaaaatttgtgctatgcaaatacaataaactggaaaaaac
                                                                                                                                                              tcgtcagcctgaacataacatccttgggattacgctccctcaaggagataagtgatggag
                                                                                                                                                                                                                 ttgagaacctagaaatcaracgcggcaggaccaagcaacatggtcagttttctcttgcag
                                                                                                                                                                                                                                   ttgagaacctagaaatcatacgcggcaggaccaagcaacatggtcagttttctctttgcag
                                                                                                                                                                                                                                                                                        aaaactgcacctccatcagtggcgatctccacatcctgccggtggcatttaggggtgact 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aaggtggcgtccgcaagtgtaagaagtgcgaagggccttgccgcaaagtgtgtaacggaa
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tgtttgggacctccggtcagaaaaccaaaattataagcaacagaggtgaaaacagctgca
                                                                                                                                          togtoagcotgaacataacatecttgggattacgctccctcaaggagataagtgatggag
                                                                                                                                                                                                                                                                                                                                                               ccttcacacatactcctcctctggatccacaggaactggatattctgaaaaccgtaaagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           taggtattggtgaatttaaagactcactctccataaatgctacgaatattaaacacttca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 981; DB 14; Length 5750; Pred. No. 8.2e-271;
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5; Indels

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818

1298

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RESULT
AAH47973
ID AAH4
XX AAH4
AC AAH4
XX O2-C
DT O2-C
DT O2-C
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Pred. No. 5.9e-113;
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Best Local :
                                                                                                                                                                                                                                                            HER4 is the fourth member of the EGFR-family of tyrosine kinases and is expressed in some human cancers and in some tissues of neuronal or muscle origin. HER4 polynucleotides, opt. labelled, are useful in assays (e.g. of HER4 mRNA to detect certain neoplasms, esp. breast carcinoma) and as primers in PCR or as probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human epidermal growth factor receptor; HER; EGF; tyrosine kinase; cancer; neuronal tissue; muscle tissue; neoplasm; carcinoma; primer; probe; PCR; ss.
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                                                                                                                                                                                                                                                                                                                                                                                        New recombinant nucleic acid expressing HER4 - a new receptor tyrosine kinase expressed in some cancer cells, and related vectors, antibodies, ligands etc. for diagnosis and treatment of
                                                                                                                                                                                                                                     Sequence 5501 BP; 1605 A; 1173 C; 1230 G; 1493 T; 0 other.
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                                14-OCT-1994;
                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                               HER4/p180erbB4; HER4; receptor tyrosine kinase;
epidermal growth factor receptor; cancer; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT18532 standard; DNA; 5501 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1784 aagatggcccaaactgtgtggaaaaatgtccagatggcttacagggggcaaacagtttca
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(BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                  25-APR-1996.
                                                                                                                                 WO9612019-A2
                                                                                                                                                                                                                                                                                                                                                                                   Receptor tyrosine kinase HER4 gene.
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                                                                 10-OCT-1995;
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Matches 991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A DNA sequence (AAT18532) codes for a novel receptor tyrosine kinase, designated HER4/pl80erDB4 or HER4 (AAR91733), which is related to epidermal growth factor receptor and which is expressed in several human cancers and in certain tissues of neuronal and muscular origin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 111-116; 203pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Culouscou J, Hellstrom I,
Shoyab M, Slegall C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           numan cancers
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680 cccccagtgactgccaccaccagtgtgccacagcctgcacaggcccccgggagagcg 739
                                                                   647 gccagactttgacaaggacggtgtgtgcagaacaatgtgacggcagatgctacggacctt 706
                                                                                                                                                                                                                                                    560 gccaaaagugtgatccaagctgtcccaatgggagctgctgggggtgccaggaggaggagaact
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                                                                                                                                                                                                                gtggacgttgccataagtcctgt---actggccgttgctggggacccacagaaaatcatt 646
                                                                                                                                                                                                                                                                                                                                                          ttgttcggaacccatggccttccaacttgactcttgtgtcaacaaatggtagttcaggat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HER4 with alternate 3'-end without AP domain
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                                                                                                                                                                              is expressed in some human cancers and in some tissues of neuronal or muscle origin. HER4 polynucleotides, opt. labelled, are useful in assays (e.g. of HER4 mRNA to detect certain neoplasms, esp.
                                                                                                                                                                                                                       This sequence is identical with that of HER4 (AAQ64896) up to nucleotide 3168, where the sequence diverges and the ORF stops after 13 amino acids, followed by an extended, unique 3'-UTR. HER4 is the fourth member of the EGFR-family of tyrosine kinases and
                                                                                                                                                                                                                                                                                                                                             New recombinant nucleic acid expressing HER4 - a new receptor tyrosine kinase expressed in some cancer cells, and related vectors, antibodies, ligands etc, for diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-1995
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                                                                                                                                   Sequence 5555 BP; 1746 A; 1054 C; 1106 G; 1647 T; 2 other;
                                                                                                                                                                                                                                                                                                  Claim 1; Fig 2A; 104pp; English
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                                                                                                                                                                breast carcinoma) and as primers in PCR or as probes.
83 agaaagtttgccaaggcacgagtaacaagctcacgcagttgggcacttttgaagatcatt 142
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                                                                                                                                                                                                                                                                    Receptor tyrosine kinase HER4 gene (alternative 3' sequence).
                                                                                                                                                                                                                                                                                                                                                                           AAT18533 standard; DNA; 5555 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1784 aagatggcccaaactgtgtggaaaaatgtccagatggcttacagggggcaaacagtttca
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding receptor tyrosine kinase, HER4 - related to human epidermal growth factor receptor, used for diagnosis and therapy of
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              simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the PA and/or at least 1 B-cell group which is cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSW, human Her2 and
                                                                                                     The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (i.e. Self-proteins), for example, human prostate specific membrane antigen (PSM), hereguin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting
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                                                                                                                                                                                                               Claim 62; Page 187-193; 220pp; English.
                                                                                                                                                                                                                                                  Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer
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                                                                                                                                                               836 tgaaccccgagggcaaatacagctttggtgccacctgcgtgaagaagtgtccccgtaatt 895
955 -- gaggaagacggcgtccgcaagtgtaagaagtgcgaagggccttgccgcaaagtgtgta 1012
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                                                                                                                                                                                                                                                                                                                                                                    cancer, the initation step for Erb-B2 gene activity is identified. This method involves determining the presence of HPBF in a biopsy from the subject, where the presence of HPBF (relative to its absence in a normal control) indicates the presence of cancer and decreased chance of long-term survival. Binding of HPBF to the promoter can be inhibited using antisense oligonucleotides or a non-genomic nucleic acid that binds to HPBF; these oligos can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Erb-B2 gene is one of the primary genes responsible for the transition of normal breast epithelial cells towards carcinoma in situ and the subsequent development of invasive and metastatic cancer. HPBF (see AAR77093-94), the Erb-B2 promoter binding prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Her-2/neu; Erb-B2; c-erbB-2; oncogene; DNA binding protein; HPBF; Erb-B2 promoter binding protein; tumour enhancer factor; breast cancer diagnosis; prognosis; antisease oligonucleotide; retro virus vector; gene therapy vector; ss.
                                                                                                                                                                                                                                                                                                                 Sequence 4530 BP; 922 A; 1382 C; 1346 G; 880 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                     expressed from retro virus or other gene therapy vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         induces cell division on binding to the promoter. In a method greater success in early identification and treatment of breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 52-54; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New purified protein binding to the ERBB2 gene promoter - to induce cell proliferation, diagnostic of breast cancer, also related antibodies, nucleic acid, assays and methods for screening
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Search completed: January 14, 2002, 20:16:54 Job time: 4314 sec

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## ALIGNMENTS

REFERENCE AUTHORS REFERENCE DEFINITION REFERENCE ACCESSION JOURNAL MEDLINE AUTHORS TITLE JOURNAL MEDLINE ORGANISM AUTHORS 3 (bases 1 to 2456)
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Harada,A.,
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High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases I to 2456) AK004911 2456 bp mRNA HTC 05-JUL-2001 Mus musculus adult male liver cDNA, RIKEN full-length enriched library clone:1300005M11, full insert sequence. Mus musculus clone: 1300005M11. Mus musculus (strain:C57BL/6J) adult male liver cDNA to mRNA, clone\_lib:RIKEN full-length enriched mouse cDNA library CAP trapper AK004911.1 GI:12836452 11042159 10349636 genes Mus

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Submitted (10-710-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-711-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                              ACAGGGCCCCGAGAGAGTGACTGTCTGGTCTGCCAAAAGTTCCAAGATGAGGCCACATGC
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Pred. No. 0;
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RESULT 2 AKO04883  CAP trapper.	Qy 1801 ggagaaaacaacacctgqtctggaagtacgcagacgccggccatgtgtgccacctgtgc 1860	Db 1876 ATCCTGGAAGGGAACCAAGGGAAGTTTGTGGAAAATTCTGAATGCATCCAGTGCCATCCA 1935  1681 gagtgccttgcctcaggccatgaacatcaccttgcacaggggaccagacactgtatc 1740  11	Oy 1501 gccacaggccaggtctgccatgccttgtgctcccccgagggctgctgggggcccggagccc 1560	Oy 1321 gtcagcctgaacataacatccttgggattacgctccctcaaggagataagtgaagat 1380	Oy 1141 ttcacacatactcctcctctggatccacaggaactggatattctgaaaaaccgtaaaggaa 1200	Oy 961 gacggcgtccgcaagtgtaagaagtgcgaagggccttgccgcaaagtgtgtaacggaata 1020
prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGACGGCCCAACTCGAGTTTTTTTTTTTTT	URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9212, Pax:81-45-	Okido, T., Owa, C., Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. TITLE Direct Submission JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (F-mail Genome-researce feet of the	TIPLE Functional annotation of a full-length mouse cDNA collection JOURNAL Nature 409, 685-690 (2001)  REFERENCE 5 (bases 1 to 2662)  AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiracka, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikogami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Mitawatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome research. 10 (11), 1757-1771 (2000)  MEDLINE 20530913  MEDLINE 20530913  PUBMED 11076861  AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	REFERENCE 2 (bases 1 to 2662)  AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayushizaki, Y.  TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes JOURNAL Genome research. 10 (10), 1617-1630 (2000)  MEDLINE 2049374  PUBMED 1042159  REFERENCE 3 (bases 1 to 2662) AUTHORS Shibata, K., Itoh, M., Aizawa, K., Negaoka, S., Sasaki, N., Carninci, P., Shibata, K., Itoh, M., Aizawa, K., Nishine, T., Harada, A., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,	SOURCE Mus musculus (strain:C57BL/6J) adult male liver cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:I300003KO7.  ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia: Sciurognathi; Muridae; Murinae; Mus. AUTHORS I (bases I to 2662) AUTHORS Carnincip and Hayashizaki, Y. TITLE High-efficiency full-length cDNA cloning JOURNAL Methods in enzymology. 303, 19-44 (1999) MEDLINE 9279233 PUBMED 10346736

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BASE COUNT
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541 cagaaccacctgggcagctgccaaaagtgtgatccaagctgtcccaatgggagctgctgg 600
                                                               762 ACTATCCAGTGGAGGGACATCGTCCAAAACGTCTTTATGAGCAACATGTCAATGGACTTA 821
                                                                                             481 agcatccagtggcgggacatagtcagcagtgactttctcagcaacatgtcgatggacttc 540
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/organism-Mus musculus"
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/strain-"C57BL/6J"
/db_xref-"Kaxon:10090"
/db_xref-"MCD:MGI:1896853"
/db_xref-"MGD:MGI:95294"
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5 hibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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                                                                                                                                        The RIKEN Genome Exploration Research Group Phase II Team and the FANTON Consortium.
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Carninci, P. and Hayashizaki, Y.
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                         Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojina, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
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61 gegagtegggetetggaggaaaagatatgeeaaggeaegagtaacaageteaegeag 120
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                                                                                                                              Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                         Similarity
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1474	TCACGCGCACTCCTCCTAGACCCACGAGAACTAGAAATTCTAAAAACCGTAAAAGGA	141	. 문
1200	ttcacaca	114	Q
1414	ACTGCACTGCATCAGCGGGACCTTGACATCCTGCCAGTGGCCTTTAAGGGGGATTCT	135	В
1140	ctgcacctccatcagtggcgatctccacatcctgccggtggcatttagggggtgact	108	õ
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1020	1 gacggcgtccgcaagtgtaagaagtgcgaagggccttgccgcaaagtgtgtaaacggaata [	96. 123	ğ 6
1234	GTGACAGATCATGGCTCATGTGTCCGAGCCTGTGGGCCTGACTACTACGAAGTGGAAGAA	117	В
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874	AGAGCCATCCGAGCAGTTGCCCCAAATGTGATCCAAGCTGTCCCAATGGAAGCTGCTC	81	В
600	ccacctgggcagctgcca	54	5
, <del>س</del> و	ACTATCCAGTGGAGGACATCGTCCAAAACGTCTTAATGAGCAACATGTCAATGGACTT	75	멅
	gcatccagtqqcqqqacataqtcaqcaqtqactttctcaqcaacatqtcqatqqoct	4 8	é
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694	CCTGTCCAACTATGGGACAAACAGAACTGGGGCTTAGGGAACTGCCCATGCGGAACTT	63	
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634	5 TTGGAGAACCTGCAGATCATCAGGGGAAATGCTCTTTATGAAAACACCTATGCCTTTAGCC	57	В
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KEYWORDS
SOURCE
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 779)
AUTHORS
Ota, T., Suzuki, Y., Saito, K., Ishii, S., Yamamoto, J., Sugiyama, T.,
Vamamoto, J., Sugiyama, T., Nishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y. and Isogai, T.,
Yamamoto, J., Sugiyama, T., Nishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y., Ishi, S.,
Yamamoto, J., Sugiyama, T., Nishikawa, T., Nakamura, Y., Sugano, S., Masuho, Y., Taba (2000)
COMMENT
Genomics Laboratory
Hellx Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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FEATURES

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BASE COUNT
ORIGIN
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1038 agactcactctccataaatgctacgaatattaaacacttcaaaaactgcacctc 1091
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Fax: 81-438-52-3952
Email: genomicsehri.co.jp
HRI human cDNA project; 5'. & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Wasuho, Y., Isogai, T.)

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute: cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1532-3 Yana, Kisarazu,
Tel: 81-438-52-3951
Fax: 81-438-52-3952
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BE272152
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Best Local Similarity
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                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
I (bases I to 960)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Contact: Robert Strausberg, Ph.D
               Unpublished (1999
                                                                                              Homo sapiens
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                                          1896 tottgaaggotgtocaacgaatgggootaagatocogtocatogooacotgggatggtggg 1955
                                                                                                                                                                                                                                    1836 cgccggccatgtgtgccacctgtgccatccaaactgcacctacggatgcactgggccagg 1895
                                                                                                                                                                                                                                                                                                                                                                                   466 CAAGACCTGCCCGGCAGGAGTCATGGGAGAAAACAACCCCTGGTCTGGAAGTACGCAGA 525
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586 TCTTGAAGGCTGTCCAACGAATGGGCCTAAGATCCCGTCCATCGCCACTGGGATGGTGGG 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 CCCTCAGGAGATAAGTGATGGAGATGTGATAATTTCAGGAAACAAAAATTTGTGCTATGC 105
                                                                                                                                                                                                                                                                                                                                                                                                                              caagacctgcccggcaggagtcatgggagaaaacacccctggtctggaagtacgcaga 1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGACGGGGACCAGACAACTGTATCCAGTGTGCCCACTACATTGACGGCCCCCACTGCGT 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aggacggggaccagacaactgtatccagtgtgcccactacattgacggcccccactgcgt 1775
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High quality sequence stop: 751
Location/Qualifiers
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3141346"
/clone=ib="IMAGE:3141346"
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/clone=ib="IMAGE:3141346"
/clone=ib="IMAGE:3141346"
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/lab_host="PH10B (phage-resistant)"
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Pred. No. 1.2e~158;
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                                                                                                                                                                                                                                                                                                              Query Match
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1400 aaaatttgtgctatgcaaatacaataaactggaaaaactgtttgggacctccggtcaga 1459
                                                                                                                                                                                                    1341 cttgggattacgctccctcaagg-agataagtgatggatggatgtgataatttcaggaaaca 1399
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                                                                                          97
                                                                                                                                                                                37 CTTGGGATTACGCTCCCTCAAGGNAGATAAGTGATGGAGATGTGATAATTTCAGGAAACA 96
                                                                                                                                                                                                                                                                                          Local
                                                                                          ANAATTTGTGCTATGCAAATACAATAAACTGGAAAAAACTGTTTGGGACCTCCGGTCAGA 156
                                                                                                                                                                                                                                                                       681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM812 row: i column: 18
High quality sequence stop: 775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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601594769F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3946761
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                          /note=*Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 264 c 320 g 202 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH108 (phage_resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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1 (bases 1 to 736)

NIH-MCC http://mgc.nc1.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Grapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
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601141568F1 NIH_MGC_9 Homo
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CDNA Library Arrayed by: The I.M.A. C.C. Consortium (Lini)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Location/Qualiflers
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/tissue_type-"adenocarcinoma cell line"
/lab_host-"DH10B (phage-resistant)"
/note-"Organ: ovary: Vector: pOTB7: Site_1: XhoI; :
ECORI: cDNA made by oligo-dT priming. Directional
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 798)
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Pred. No. 1.7e-149;
0; Mismatches 6;
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TITLE
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Best Local Similarity
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241 accatccaggaggtggctggttatgtcctcattgccctcaacacagtggagcgaattcct 300
                                                                                                                                                                                                                                                                                                                                                                                                                      308 GTCCTTGGGAATTTGGAAATTACCTATGTGCAGAGGAATTATGATCTTTCCTTCTTAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 GTCTTATCTAACTATGATGCAAATAAAACCGGACTGAAGGAGCTGCCCCATGAGAAATTTA 547
                                                                                                                                                      361 gtcttatctaactatgatgcaaataaaaccygactgaaggagctgcccatgagaaattta 420
                                                                                                                                                                                                            428 TTGGAAAACCTGCAGATCATCAGAGGAAATATGTACTACGAAAATTCCTATGCCTTAGCA 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 GCGAGTCGGGGCTCTGGAGGAAAAGAAGTTTGCCAAGGCACGAGTAACAAGCTCACGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 gcgaqtcgggctctggaggaaaagaaagtttgccaaggcacgagtaacaagctcacgcag 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gtccttgggaatttggaaattacctatgtgcagaggaattatgatctttccttcttaaag 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1042 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 a
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/db_xrefr"taxon:9606"
/clone-*TMAGE:2370045"
/clone_*Iib-"Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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Matches 624;

Local

Similarity

29.8%; 98.4%;

Conservative

0; Mismatches Score 606.8; DB 10; Pred. No. 1.6e-147;

Indels

3; Gaps

1422 aatsaactggaaaaactgtttgggacctccggtcagaaaaccaaaattataagcaacag 1481

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 634)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM812 row: e column: 17
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                                                                                                     160 a
                                                                                         /tissue_type="adenocarcinoma cell line"
/lab_host="DHPOB (phage-resistant)" | Site_1: XhoI; Site_2: /note="organ: ovary; Vector: poTBP; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 169 c 188 g 117 t
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3948664"
/clone_lib="NIH_MGC_9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Length 634;
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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI740805 BD MRNA EST 19-DEC-1999 wg24008.x1 Soares_NSF_F8_9N_OT_PA_P_51 Homo sapiens cDNA clone IMAGE:2366031 3' similar to gb:K03193 EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN); , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-remail.nih.gov
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.linl.gov) for further information.
INSEC Consortium (info@image.linl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata: Craniata: Vertebrata; Euteleostomi; Mammalia; Eutheria; erimates; Catarrhini; Hominidae; Homo. 1 (basea to 805) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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Location/Qualifiers
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                                       /organisma"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2366031"
/clone=_lib="Soares_NSF_F8_9W_07_PA_P_S1"
/lab_host="DH10B"
       /note-*Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
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                                                                                                                                                                                                                                             694 CAGAACCACCTGNGCAGCTGNCAAAAGTG-GATCCCAGCTGTCCCAATGGGAGCTTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 accatccaggaggtggctggttatgtcctcattgccctcaacacagtggagcgaattcct 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 GTCCTTGGGAATTTGGAAATTACCTATGTGCAGAGGAATTATGATCTTTCCTTCTTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 gtccttgggaatttggaaattacctatgtgcagaggaattatgatctttccttcttaaag 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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A1935313 757 bp mRNA EST 08-MAR-2000 wp16907.x1 NCI_CGAP_LI19 Homo sapiens cDNA_clone IMAGE.2455052 3' similar to gb:K03193 EPIDERWAL GROWTH FACTOR RECEPTOR PRECURSOR
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Equal amounts of plasmid DNA from five normalized
Ilibraries were mixed, and as circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneries: Soares where pool 1:
1039384-310319, 323208-325895 Soares where pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150007, 151176-152327 Soares wbleff bool 1:
1758280-760531, 320186-322823, 325280-32563 Soares wbhor
15001, 121720-726007, 739080-740999 Subtraction by Bento
Scares and M. Patting horaldo.
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Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 GTCCTTGGGAATTTGGAAATTACCTATGTGCAGAGGAATTATGATCTTTCCTTCTTAAAG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 gcgagtcgggctctggaggaaaagaaagtttgccaaggcacgagtaacaagctcacgcag 120
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                                                                                                                                                                                                                                                                          TTGGGCACTTTTGAAGATCATTTTCTCAGCCTCCAGAGGATGTTCAATAACTGTGAGGTG 325
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
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Insert Length: 1220 Std Error: 0.00
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/note-"Organ: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pT7T3 vector.
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/db_xref="taxon:9606"
/clone="IMAGE:2465052"
/clone_lib="NCI_CGAP_Lu19"
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Pred. No. 7.9e-141;
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he Not I and Eco RI sites of the modified
Library went through one round of
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM190 row: a column: 11
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NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: ATCC
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/tasue_tpe="neuroblastoma"
/lab_host="bH10B (phage-resistant)"
/lab_host="bH10B (phage-resistant)"
/note="forgan: brain; Vector: pOTB7; Site_1: xhoI; Site_2: note="forgan: brain; Vector: poTB7; Site_1: xhoI; Site_2: cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACCARG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZA-CDMA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (Dases 1 to 1031)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                 found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov
Plate: LLAM11328 row: a column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                         602980849F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5133589 5',
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                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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                   quality sequence stop: 808
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Pred. No. 1.8e-128;
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acagatcacggctcgtgcgtccgagcctgtggggccgaccactatgagatggaggaagac
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                                                      GAAGGGAAGTACAGCTTTGGTGCCACCTGTGTGAAGAAGTGCCCCCGAAACTACGTGGTG
                                                                                                                           GGGCCCCGAGAGAGTGACTGTCTGGTCTGCCAAAAGTTCCAAGATGAGGCCACATGCAAA
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/Clone_lib="NGI_CGAP_Li9"
/Clone_lib="NGI_CGAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1:
Site_2: Sali; Cloned unidirectionally, Primer: Oli
Average insert size 1.9 kb. Constructed by Life
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77.5%;
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Searched:
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SUMMARIES

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1 Similarity 100.0%;
72; Conservative (
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1347)
Haley, J.; Whittle, N., Bennet, P., Kinchington, D., Ullrich, A. and
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 human
                                                                                                                                                                                                                                                                                                     The human EGF receptor gene: structure of the 110 kb locus and
                                                                                                                                                                                                                                                                                                                    Waterfield, M.
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                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="A432"
/clone="LIII"
644 . 649
                                                              /note-*TC rich regulatory sequence"
778. .793
/note-*TC rich regulatory sequence"
797. .813
                                                                                                                                              /note="f
731. .74
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253 c
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466. .560
                                       /note="TC rich regulatory sequence" 808. .813
                                                                                                                     /note="TC rich regulatory sequence"
752. .766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GDB:G00-120-610"
/product="EGF receptor"
/protein_id="AAA52370.1"
/db_xref="G1:553272"
/translation="MRPSGTAGAALLALLAALCPASRALEEKK"
                                                                                                                                                                                                                                       Location/Qualifiers
1. .1347
               /note="pot.
839. .>1189
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/db_xref="taxon:9606"
                                                                                                                                                          pot.Spl binding site"
                         Sp1 binding site"
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Pred. No. 4.1e-07;
); Mismatches 0;
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                          AUTHORS
TITLE
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Best Local :
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U48722
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GCGAGTCGGGCT 1173
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1593)
1 (base
                                     Reiter, J.L.
Direct Submission
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Submitted (07-FEB-1996) Jill L.
                                                                                                                 (bases 1 to 1593)
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1248. .1251
/note="pot. Spl binding site"
1286. .1291
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839. .>1189
839. .>1347
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/note="pot. Spl binding site"
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1102. .>1189
/note*"A431 EGF receptor (AA 1 - 29) (1189 is 1st base in codon)"
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999. .>1347
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992. .>1347
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979. .>1347
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899. .>1347
/note="altern. primary transcript"
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/translation-"MRPSGTAGAALLALLAALCPASRALEEKK"
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/db_xref="GI:31119"
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939. .>1347
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Pred. No. 3e-07;
); Mismatches
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Reiter, Biochemistry and Molecular
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polyA_signal
polyA_site
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                                                                                                                                                                                                                                                                                406
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                         /note="encodes Asn-linked glyo
1452, 1456
/gene="EGFR"
/note="5" splice donor site"
1463, 1569
1537, 1542
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1298. .1306
/gene="EGFR"
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STQNRDTVSSDFLSNMSMDFQNHLGSCQKCDPSCPNGSCWGAGEENCQKLTKTTCAQQ
CSGRCRGKSPSDCCHNQCAAGCTGPRESDCLVCRKFRDEATCKDTCPPLMLYNPTTYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"epidermal growth factor receptor precursor"
/protein_id="AAC50802.1"
/protein_id="AAC50802.1"
/db_xref="GI:1628550"
/tanslation="MRPSGTAGAALLALLAALCPASRALEEKKVCQGTSNKLTQLGTF
/translation="MRPSGTAGAALLALLALLAALCPASRALEEKKVCQGTSNKLTQLGTF
EDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLE
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245. .1462
                                                                                                                                                                                                                                                                                                                                                                                                     /note="encodes Asn-linked glycoslyation site"
1325. .1333
/gene="EGFR"
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767. .775
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KVCNGIGIGEFKDSLSINATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQEL
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/db_xref="taxon:9606"
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                                                                                                                                                                                               Score 72; DB 9;
Pred. No. 2.8e-07;
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KEYWORDS
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1 (bases 1 to 1866)
1 lekis,J.V., Stark,B.C. and Scoccia,B.
Possible role of variant RNA transcripts in the regulation of epidermal growth factor receptor expression in human placenta Mol. Reprod. Dev. 41 (2), 149-156 (1995)
95382957
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                                                                                                                                                                  Direct Submission
Submitted (25-MAR-1997) Obstetrics & Gynecology, University
Illinois at Chicago, 820 S. Wood Street, Chicago, IL 60612,
please also see Ilekis, J. in RK Miller, HA Thiede (eds):
'Molecular Biology and Ceil Regulation of the Placenta.' Nev
Plenum, 103-117, 1991.
                                                                                                                                                                                                                                                                                    2 (bases 1 to 1868)

1 (bases 1 to 1868)

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2 (bases 1 to 1868)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="TEGFR; the calculated molecular weight of the nascent protein is approximately 42 kD (includes signal peptide at amino acid positions 1-24); the molecular
                                                    /tissue_type="placenta"
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504. .1721
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/db_xref="taxon:9606"
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1 (bases 1 to 2643)

Merlino,G.T., Ishii,S., Whang-Peng,J., Knutsen,T., Xu,Y.-H., Clark,A.J.L., Stratton,R.H., Wilson,R.K., Ma,D.-P.P., Roe,B.A., Hunts,J.H., Shimizu,N. and Pastan,I.

Structure and localization of genes encoding aberrant and normal epidermal growth factor receptor RNAs from A431 human carcinoma
                                                                                                                                                                                                                                                                    A draft entry and printed copy of this sequence were kindly provided by G.Merlino (07-OCT-1985).
                                                                                                                                                                                                                                                                                                               Mol. Cell. Biol. 5 (7), 1722-1734 (1985) 85267689
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Human aberrant (short) epidermal growth factor receptor mRNA.
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EDHFL5LQrmfnncevvignleityvqnnydlsflktqovacyvltalntveriple
NLQIIRQnmyyensyalavlsavdankrglkelpmrnlqsilhgavprsnnpalcnve
SIQWRDIVSSDFLSNMSMDFQNHLGSCQKCDpSGCPGAGEELQGKLTKIICAQQ
CSGRCRKSPSDCCHNQCAAGCTGPRESDCLYCRKFRDEATCRDTCPPLMLYRGTTYQ
MDVNPEGKYSPSDCCHNQCAAGCTGPRESDCLYCRKFRDEATCRDTCPPLMLYRGTTYQ
MDVNPEGKYSPSDCCHNQCAAGCTGPRESDCLYCRKFRDEATCRDTCPPLMLYRGTTYQ
KVCNGIGIGEFRDSLSINATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQEL
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                                                                              /note="EGFR(S) mRNA; G00-120-610"
1. .2643
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/db_xref="taxon:9606"
/map="7p13-p12"
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'note-"aberrant epidermal growth factor receptor"
                    'gene="EGFR"
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704 a 693 c 699 g 547 t
Chromosome 7; 493 bp upstream of RsaI site
                                                                                                                                                                                                                                                         Clinic,
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/protein_id="AAA52371.1"
/db_xref="GI:181985"
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EDHFLSLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQETAGGYVLIALNTVERIPLE
RUQILERGNMYYENSYALAVLSNYDANKTGLKELPMRNLGEILHGAGGYVLIALNTVACRVERIPLE
NLQILERGNMYYENSYALAVLSNYDANKTGLKELPMRNLGEILHGAGGYVLTANDALCNVE
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RSLKEISDGDVIISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSCKATGQVCHA
LCSPEGGWQPERPROCYSCREVAVSRGREGVDKCNLLEGEPREFYENSECIQCHPECLIPQA
MNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVMGENNTLVWKYADAGHVCHLCHPNC
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CSGRCRGKSPSDCCHNQCAAGCTGPRESDCLVGRKFRDEATCKDTCPPLHLYNPTTYQ
MDVNPEGKKSFGATCVKKCPRNYVVTDHGSCVRACCADSYBMBEDGVRKCKEGCPCR
KVCNGIGIGEFKDSLSINATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQEL
/gene="EGFR"
246. .2363
                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                         00 First St. SW, Rochester,
Location/Qualifiers
                                                      /tissue_type="placenta"
l. .2864
                                                                                                       /map="7p11.2-p12"
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Pred. No. 2.4e-07
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                                                                                                                                                                                                                                                         MN 55905, USA
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306 GCGAGTCGGGCT 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 gcgagtcgggct 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 363)
Pippig,S.D. and Veres,G.
Selectable cell surface marker genes
Patent: WO 0136659-A 1 25-MAY-2001;
Docation/Qualifiers
1. 3633
                                                                                                                                                                                                                                                                                                                                                               AX179384 3633 bp DNA
Sequence 1 from Patent WO0136659.
AX179384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [ Similarity
72; Conserv
                                                                                                                                                                                                                                                         unidentified
                                                                                                                                                                                                                                                                                  unidentified
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                                                                                                                                                                                                                             unclassified
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2864
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DILKTYKEITGELLIQAWPENRTDLHAFENLEIIRGEKGHGQFSLAVVSLNITSLGL
RSLKEISDGDVIISGKNLCYANTINKKLFGTSGOXTKIISHRGENSCKATGOVCHA
LCSPEGCWGPERDCVSCRNVSRGRECVDKCNLLEGEFREFVENSECIQCHPECLPQA
MNITCTGRRGDNCIQCAHYIDGPHCVKTCPAGYMGENNTLYWKYADAGHYCHLCHPNC
TYGPGNESLKAMLFCLFKLSSCNQSNDGSVSHQSGSPAAQESCLGWIPSLLPSEFQLG
WGGCSHLHAWPSASVIITASSCH*
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2832. .2837
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/product="truncated epidermal growth factor receptor
precursor"
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/db_xref~"GI:12002212"
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829 c
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2847
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/note="ERBB1; alternative transcript encoding only the
/organism="unidentified"
/db_xref="taxon:32644"
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100.0%; Pred. No. 2.3e-07;
tive 0; Mismatches 0;
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SOURCE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Draft entry and computer-readable sequence for [Unpublished (1990)] kindly submitted by J.D.Haley, 12-SEP-1990.
Oncogene Science Inc.
350 Community Drive Manhasset, NY 11030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hum. Mol. Genet. 1 (2), 135 (1992)
93244774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Two chromosome 7 dinucleotide repeat polymorphisms at gene loci epidermal growth factor receptor (EGFR) and pro alpha 2 (1) collagen (COL1A2)
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Haley, J. D. and Waterfield, M. D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell surface receptor; epidermal growth factor Human DNA, clone LIII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contributory effects of de novo transcription and transcript termination in the regulation of human factor receptor proto-oncogene RNA synthesis J. Biol. Chem. 266 (3), 1746-1753 (1991) 91107677
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1007 c 953 g 7
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a 1219 c
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/note="G00-120-610"
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/db_xref="GI:553271"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="7p13-p12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="LIII"
                                                                                                              /partial
                                                                                                                                                                   /translation~"MRPSGTAGAALLALLAALCPASRALEEKK"
                                                                                                                                                                                                                                                                                     /codon_start=1
/db_xref="GDB:G00-120-610"
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Pred. No. 2.1e-07;
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BASE COUNT ORIGIN

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polyA\_site polyA\_site polyA\_site polyA\_site polyA\_signal polyA\_signa mat\_peptide

receptor.

06-MAR-1995

0; Gaps

0;

epidermal

growth.

sig\_peptide

Query Match Best Local :

Local

Matches

REFERENCE AUTHORS TITLE

FEATURES

KEYWORDS SOURCE

ORGANISM

RESULT AX179384

8

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DEFINITION ACCESSION

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                                                                                                                                                                                                                                                                                                                                             49 Convent Dr., 1
Tel: 3014020201
Fax: 3014024735
                                                                                                                                                                                                                                                                                                                                                             GDB_DSEG: EGER
CONTRACT: EFIC D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08,
Tel: 3014020201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3888)

Bouffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F., Weintraub,L.A., Mohr-Tiowell,R.M., Peluso,D.C., Fulton,R.S., Leckle,M.P. and Green,E.D.

A collection of 1814 human chromosome 7-specific STSs Genome Res. 7 (1), 59-64 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human chromosome 7 STSs (1997)
Unpublished (1997)
Synonyms: EGFR
GDB: GDB:196214
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                                                                       Buffer:
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                                                                                                                                                                          Protocol
                                                                                                                                                                                                                                                                                                       Primer B: TTCTTCTGCACACTTGGCAC
                                                                                                                                                                                                                                                                                                                    Email: egreen@nhgri.nih.gov
Primer A: GTTTGAAGAATTTGAGCCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                         size: 119
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            MgCl2:
KCl:
Tris-HCl:
NH4Cl:
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Polymerization:
PCR Cycles:
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Total Vol:
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92 degrees C for
60 degrees C for
72 degrees C for
35
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: 0.05 units/ul
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0.17 minute(s)
1.00 minute(s)
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                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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               61 gcgagtcgggct 72
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                                                                                                                             Local
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72; Conserv
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                                                                                                                                                                                                                                                                      1 (bases 1 to 5532)
King C.Richter, Kraus, M.H. and Aaronson, S.A.
erbB-2 gene segments, probes, recombinant DNA and kits for detection
                                                                                                                                                                                                                                                           Patent: US 5985553-A 3 16-NOV-1999;
                                                                                                                                                                                                                                                                                                                                              Unknown
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Sequence 3 from patent US 5985553.
AR086089
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                                                                                                                                                                                                                                                                                                                               Unclassified.
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                                                                                                               Conservative
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2338. .2456
/gene="EGFR"
2338. .2359
2338. .2359
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a 1219 c 1101
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1 1484 c 1337 g
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/db_xref="taxon:9606"
/map="7"
                                                                                                                                                                                                                             Location/Qualifiers
1. .5532
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Pred. No. 1.8e-07;
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RESULT 12

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1 (bases 1 to 5532)

Ullrich, A., Coussens, L., Hayflick, J.S., Dull, T.J., Gray, A., Ullrich, A., Schlessinger, J., William, J., William, Y., Libermann, T.A., Schlessinger, J., William, W. Lee, J., Yarden, Y., Libermann, T.A., Schlessinger, J., and W. Lee, J., Yarden, Y., Libermann, T.A., Schlessinger, J., and W. Lee, J., Yarden, Y., Libermann, T.A., Schlessinger, J., and W. Lee, J., Yarden, Y., Libermann, T.A., Schlessinger, J., and W. Lee, J., Yarden, Y., Libermann, T.A., Schlessinger, J., and W. Lee, J., Yarden, Y., Libermann, T.A., Schlessinger, J., and W. Lee, J., Yarden, Y., Libermann, T.A., Schlessinger, J., and W. Lee, W. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cel Nature 309 (5967), 418-425 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Downward, J., Mayes, E.L., Whittle, N., Waterfield, M.D. and Seeburg, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Euthería; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
187, .258
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/translation="mrPSGTAGAALLALLAALCPASRALEEKKVCQGTSNKLTQLGTF
EDHFUSLQRWENNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLE
                                                                                                                                                                                                                                                                                                                          /note="Asn-linked glycosylation site"
997. .1006
                                                                                                                                                                                                                                                                                                                                                                                /note="
772. .7
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568. .576
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RTPLLSSLSATSNNSTVACIDRNGLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTFLP
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/protein_id="CAA25240.1"
/db_xref="GI:757924"
                                                                                                     /note~"Asn-linked glycosylation site"
1506. .1514
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1267. .1275
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                                                              1506. .1514
/note="Asn-linked glycosylation site"
                                                                                                                                                                                   'note="Asn-linked glycosylation site"
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                    'note="Asn-linked glycosylation site"
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                                                                                                                                                  3 (bases 1 to 177998)
Waterston,R.H.
Direct Submission
Submitted (05-MAR-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                 Waterston, R.H.

Direct Submission
Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoka: Metazoa; Chordata; Craaiata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 17798)
Suiston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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AC006977
MO 63108, USA
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1924. .3732
/note="v-erb B homology"
1993. .2001
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3313. .3321
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Pred. No. 1.8e-07;
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Direct Submission
Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
Oniversity, 4444 forest Park Avenue, St. Louis, Missouri 63108,
On Sep 28, 1999 this sequence version replaced gi:4662682.
Genome Center
Genome Center
Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                       The clone sequenced to the left is RP4-791C19, 200 bp overlap. Actual start of this clone is at base position 80354 of RP4-791C19; actual end is at base position 177998 of RP5-1091E12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE INFORMATION:
This clone was derived from human PAC library RPCI-5, prepared by Pleter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from the companion of the companion of the library is from the library in the library is from the library in the library is from the library in the library in the library is from the library in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGSI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. Por additional Information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR, send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone RP5-1091E12 from base position 192688 to 192794 is an approximate representation of a tandem repeat. There are approximately 800 bases of this tandem missing according to the restriction digests: ecorRV band size real at 5047, insilico at 4288; hindili band size real at 10980, insilico at 10434; bamhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one male donor.
The clowe may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send
mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAPPING INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted:
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                             /rpt_family="Alu"
2744. .3029
                                                                                          /rpt_family="L1"
2566. .2617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCYPAC:
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/clone="RP5-1091E12"
                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
   /rpt_family-"Alu"
                                                                                                                                                                                             clone_lib="RPCI-5"
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3586. .40
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13289
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/note="similar to EST AI263609 (NID:g3871812) qq89g02.xl"

9298. .9472
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/note-"match to EST AI935313 (NID:g5674183) wpl6g07.x1"
9258. .9472
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9010. .9102
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4729. .5555
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4417. .4726
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4303. .439
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                                                                                              /rpt_family~"(TA)n"
18838. .18872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match to EST AI554567 (NID:g4486930) tn25f08.x1" 9231. .9472
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9231. .9472
                                /rpt_family~"AT_rich"
18985. .19279
                                                                                                                                                                                                                                 17959.
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15231, .15735
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13475. .13
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u120a11.y1"
rpt_family="Alu"
                                                                                                                                                                                             note="match to EST AA640700 (NID:g2565950) nr22f01.rl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="match to EST AA768080 (NID:g2819095) nv96h04.sl"
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/note="similar to EST R35665 (NID:g792566) yh90f01.s1"
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1 Similarity 100.0%; Pred. No. 5.5e-08;
72; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                ullrich, A., Coussens, L., Hayflick, J.S., Dull, T.J., Gray, A., Tam, A. W., Lee, J., Yarden, Y., Libermann, T.A., Schlessinger, J., Downward, J., Mayes, E.L.V., Whittle, N., Waterfield, M.D. and Seeburg, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF288738 197496 bp DNA PRI 26-JAN-2001
Homo sapiens epidermal growth factor receptor (EGFR) gene, complete
cds, alternatively spliced; and 5S ribosomal RNA gene, complete
                                                                                                                                                                            Merlino,G.T., Ishii,S., Whang-Peng,J., Knutsen,T., Xu,Y.-H., Clark,A.J.L., Stratton,R.H., Wilson,R.K., Ma,D.P., Roe,B.A., Hunts,J.H., Shimzu,N. and Pastan,I. Structure and localization of genes encoding aberrant and normal epidermal growth factor receptor RNAs from A431 human carcinoma
                                                                                                                                                                                                                                                                                                                                         Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cells Nature 309 (5967), 418-425 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 9385 to 197496)
3 (bases 9385 to 146950)
Reiter, J.L. and Maihle, N.J.
A 1.8 kb alternative transcript from the human epidermal growth
A 1.8 kb alternative transcript from the human epidermal growth
factor receptor gene encodes a truncated form of the receptor
Nucleic Acids Res. 24 (20), 4050-4056 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                     Cell. Biol. 5 (7), 1722-1734 (1985)
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20169. .20170
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27748. .27851
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24646. .24871
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Eley,G., Frederick,L., Wang,X.Y., Smith,D.I. and James,C.D.
3' end structure and rearrangements of EGFR in glioblastomas
Genes Chromosomes Cancer 23 (3), 248-254 (1998)
99005167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-JUL-2000) Blochemistry and Molecular Biology, Mayo Clinic, 200 First St. SW, Nochester, MN 55905, USA Part of this sequence is also presented in GenBank Accession number AC006977, produced as a collaborative effort between the Genome Sequencing Center at the Washington University School of Medicine and J.L. Reiter and G.D. Eley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reiter, J.L., Threadgill, D.W., Eley G.D., Strunk, K.E., Danielsen, A.J., Schehl Sinclair, C., Pearsall, R.S., Green, P.J., Yee, D., Lampland, A.L., Balasubramentam, S., Crossley, T.D., Magnuson, T.R., James, C.D. and Maihle, N.J. Comparative genemic sequence analysis and isolation of human and mouse alternative egfr transcripts encoding truncated receptor
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6 (bases
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AB025197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kondoh, S. K. and Aktyama, N.
Rat EGFR promoter from NRK cells
Published Only in DataBase (1999) In press
2 (bases I to 1858)
Kondoh, S. K. and Aktyama, N.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus cell_line:NFK DNA.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB025197.1 GI:4586455
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1775, .>1858
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1775. .1858
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144118...144259,145937...146053,146640...146766,
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/protein_id="BAA76391.1"
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Pred. No. 5.3e-08;
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ORIGIN

Query Match 60.8%; Score 43.8; DB 10; Length 1858; Best Local Similarity 76.1%; Pred. No. 0.57; Matches 54; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

DЬ

Search completed: January 14, 2002, 20:13:57 Job time: 4182 sec

61 gcgagtcgggc 71

Дb 1835 GCAGGTGGGGC 1845

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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N_Geneseq_1101:*

/SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
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4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
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15: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search time 159.75 Seconds (without alignments) 386.400 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human cytokine rec Human epidermal gr Epidermal growth f Epidermal growth f Nucleotide sequence CDNA sequence enco Human EGF receptor PRLD3D4 construct. PRLD2D3D3.Apal.con EGF receptor relative Nucleotide sequence	AAA111949 AAS01680 AAV06408 AAV66408 AAF85332 AAC61552 AAZ23954 AAQ43814 AAQ43813 AAQ43813 AAQ43813 AAQ43813	21 22 22 22 22 21 14 14 22 22 21	1200 1663 1868 3633 3818 5532 5750 6207 6207 6274 58857	100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 83.3 83.3	72 72 72 72 72 72 72 72 60 60 43.8	C 110 8 7 6 5 5 4 3 2 2 1
Description	ID		Query Match Length DB	Query	Score	Result No.
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45	44	43	42	41	40	39	38	37	36	<u>ყ</u>	34	<u>ω</u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
26.4	26.4	26.6	26.6	26.6	26.6	26.8	26.8	27	27	27	27	27	27	27	27.2		27.4	27.4	27.4	27.4	27.8	27.8	28	28	Θ	æ	8	8	8	8	28.6	8	8
7	7	9	9	9	Ω	Ν	N	v	S	37.5	G	Ç	5	S	æ	-	1	Н	+-4	Н	9	9	9	9	IJ	42-	4	7	39.7	39.7	39.7	39.7	39.7
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22	16	19	21	21	19	20	19	18	21	21	21	20	22	18	22	22	19	19	19	19	21	21	13	15	22	20	20	22	21	19	17	21	19
AAH33653	AAT05324	AAV62176	AAA14651	AAC75821	AAV28875	AAX03728	AAV46425	AAV04449	AAA50532	AAA50497	AAA90932	AAX26234	AAH34426	AAV04448	AAI64000	AAA09686	AAV49510	AAV49625	AAV49626	AAV62138	AAA58471	AAC44552	AAQ22957	AAQ70935	AAD13350	AAX15110	AAZ20131	AAF30870	AAA13905	AAV23494	AAT28293	AAA13900	AAV23486
Human colon cancer	Human prostacyclin	HSV-2 strain SB5 C	Nucleotide sequenc	Human ORFX ORF1376	Candida antartica	Zea mays cinnamyl	Maize cinnamoyl Co	Mouse programmed c	DNA encoding angio	DNA encoding trunc	Human W10 protein	Truncated p27/p16	Human colon cancer	Mouse programmed c	Human polynucleoti	HSV-2 immediate ea	Mycobacterium sp.	Mycobacterium tube	Mycobacterium tube	HSV-2 strain SB5 C	Nucleotide sequenc	Zea mays DNA fragm	Sequence of beta-1	Human epidermal gr	Human secreted pro	Transcriptional re	Human CDK-inhibito	Pseudomonas alcali		Pseudomonas Xpc, O	Mouse IRS-2 cDNA.		Pseudomonas XcpV s

## ALIGNMENTS

AA1	AA11949
U	AAA11949 standard; DNA; 1200 BP.
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Ċ	AAA11949;
×	
Ä	01-AUG-2000 (first entry)
×	
ট্য	Human cytokine receptor gene fragment DNA
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Cytokine receptor; cell proliferative disease; diagnosis; primer; cytosine methylation; psoriasis; chronic rheumatoid arthritis; arteriosclerosis; blood vessel re-narrowing; diabetic retinopathy; premature neonate retinopathy; tumor; ss.

17-SEP-1999; Homo sapiens. (KYOW ) KYOWA HAKKO KOGYO KK 18-SEP-1998; 30-MAR-2000. WO200017339-A1 98JP-0265089. 99WO-JP05069

WPI; 2000-283572/24. Нопита Ү, Oyama N, Sato K;

blood for genomic DNA extraction Rapid and highly reproducible diagnosis of cell proliferative diseases e.g. chronic rheumatoid arthritis and psoriasis, using particularly blood for genomic DNA extraction -

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RESULT
AAS01680
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atches
                                                                                                                                                                                                                                                                                                                                                                                                     Human; T-type calcium channel; CACNAIG; cytosine methylation; CpG island; cellular proliferative disorder; colorectal cancer; age related disease; apolipoprotein B; APOB; caudal type homeobox transcription factor 2; CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBM1; G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B'; HSPA6; RasGAP-related protein; IQGAP2; proteinsas-activated receptor 2; PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL; patched A; patched B; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4; chromosome 7p12; ds.
The present sequence for epldermal growth factor receptor (EGFR)
                                Claim 32; Fig 4B; 125pp; English.
                                                               New nucleic acid molecule for use as a marker for screening cancer, comprises the coding region for a T-type calcium channel and regulatory sequences associated with the channel
                                                                                                                                                                                                                                                                      14-SEP-2000; 2000WO-US25479
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel rapid and highly reproducible method for diagnosis of a cell proliferative disease, comprising analyzing the extent of methylation of cytosine residue in a region participating in the chromosome DNA-related expression of a cytokine receptor gene. The method is used for the diagnosis for psoriasis, chronic rheumatoid arthritis, arteriosclerosis, blood vessel re-nearrowing, diabetic retinopathy, premature neonate retinopathy or solid tumor wising body fluids or tissues, particularly blood for genomic DNA extraction. This sequence represents fragment of the human cytokine receptor described in
                                                                                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                         15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human epidermal growth factor receptor (EGFR) CpG island.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS01680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS01680 standard; DNA; 1663 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                    WPI; 2001-244777/25.
                                                                                                                                                                      ISSa
                                                                                                                                                                                                                                                                                                                                         WO200119845-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1200 BP; 195 A; 430 C; 354 G; 213 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                         99US-0398522
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CpG island is used to study the methylation state of EGFR which maps to chromosome 7p12. The methylation state of specific regions within CpG islands associated with a novel T-type calcium channel CACNAIG gene correlate with several cancerous phenotypes involving various tissue and cell types. Since aberrant methylation of normally unmethylated CpG islands is often observed in immortalised and transformed cells. CACNAIG is implicated in cellular proliferative disorders e.g. leukaemia, CACNAIG is implicated in cellular proliferative disorders e.g. leukaemia, colorectal, lung, breast and other cancers. The nucleic acid coding for CACNAIG is useful as a marker for screening cancer and age related diseases. A diagnostic kit containing nucleic acid, where the primer hybridises with a target polynucleotide sequence (AASO1627-AASO1676), can be used for detecting aberrant methylation. The CpG island sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AASO1677-AASO1692) are selected from genes encoding CACNAIG, apolipoprotein B (APOB), caudal type homeobox transcription factor 2 (CDX2), epidermal growth factor receptor (EGFR), fibrilin-1 (FBN1), G protein-coupled receptor 37 (GPR37), heat shock 70KD protein GHSP70B'; HSPA6), RasGAP-related protein (IGARP2), klotho (KL), proteinase-activated receptor 2 (PAR2), paired-like homeodomain transcription factor 2 (PTMX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1; SDC4) or a MINT31 sequence.
                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                           Epidermal growth factor receptor-like protein; diagnosis; cancer; hyperproliferative disease;
              (ILEK/) ILEKIS J V
                                               31-MAY-1996;
                                                                                                               13-JAN-1998
                                                                                                                                                                                          mat_peptide
                                                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV06408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV06408 standard; DNA; 1868 BP
                                                                                                                                             US5708156-A
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                            Epidermal growth factor receptor-like protein (TEGFR) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1663 BP; 199 A; 684 C; 543 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           606 gcgagtcgggct 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative (
                                             96US-0658883.
                                                                               96US-0658883.
                                                                                                                                                                                          /*tag= b
/oote= "putative signal peptide"
576..1718
                                                                                                                                                                                                                                              /product= TEGER 504..575
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                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 72; DB 22;
Pred. No. 7.4e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              TEGFR; human; antibody ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1663;
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      XEXEXEX
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                       19-NOV-1999; 99US-0166594
19-NOV-1999; 99US-0444038
30-MAR-2000; 2000US-0539248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Epidermal growth factor receptor 1; EGFR1; cell surface marker; protein-tyrosine kinase receptor; PTKR; immunoselection; gene therapy; bone marrow transplant; graft facilitation; immune reconstitution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of wild type EGFR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF85332 standard; DNA; 3633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1868 BP; 449 A; 554 C; 494 G; 371 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide related to epidermal growth factor receptor -corresponding DNA and antibody useful for cancer diagnosis
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P-PSDB; AAW33737.
Pippig SD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF85332;
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                                                         (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN
                                                                                                                                                                                                                                                                                       17-NOV-2000; 2000WO-EP11474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_except= "(pos: 1618..1620, aa: Asn)"
/product= "EGFR1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Pred. No. 7.4e-10;
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RESULT
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PAXRARRAN PAXRAR
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Best Local Similarity 100.0%;
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                                                      07-JUN-1995;
01-JUN-1990;
08-SEP-1989;
11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            any nerve growth factor receptor(s) (NGFR). The method uses mutated PTKR as a cell surface marker, and is useful for identifying genetically modified cells, especially immunoselection of transduced mammalian cells, and for identifying mammalian cells expressing a protein of interest. The genetically modified marked cells may be used in an autologous or allogeneic setting e.g. gene therapy for bone marrow transplants, graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a human epidermal growth factor receptor 1 (EGFRI). EGFR is a protein-tyrosine kinase receptor (PTKR). The specification describes a method for identifying genetically modified mammalian cells. The method uses a mutated PTKR nucleic acid which comprises a modification to the intracellular and extracellular domains, or comprises a modification to the intracellular domain and excludes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying genetically modified mammalian cells for use in e.g. bone marrow transplants, comprises use of mutated protein-tyrosine kinase receptor nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glioma; brain; breast tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequence encoding an epidermal growth factor receptor.
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P-PSDB; AAB68420.
(UYDU-) UNIV
                                                                                                                                                                                                        09-MAR-1999;
                                                                                                                                                                                                                                                                 03-OCT-2000
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DUKE
                                                                               95US-0479808.
90US-0531410.
89US-0404226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; epidermal
lung tumour; ss.
                                                                                                                                                                                                     99US-0264723
                                                                                                                                                                                                                                                                                                                                                                              /*tag~ a
/product~ "epidermal growth factor receptor"
/note~ "no termination codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 187..3817
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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AAZ23954
ID AAZ2
XX
AC AAZ2
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AC AAZ2
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AC BA-C
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DT 28-C
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DE Hume
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Hume
В
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Best Local S
                                                                                                  21-OCT-1987;
01-NOV-1991;
05-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a method for diagnosing glioma in a brain cell sample suspected of being cancerous. The method comprises detecting the presence of a nucleic acid encoding an epidermal growth factor receptor (BGFR) mutant protein type II. Deletions in the EGFR gene are found in many gliomas. breast tumours and lung tumours. The method is useful for diagnosing gliomas, breast tumours and lung tumours. The present sequence encodes a normal EGFR polypeptide.
                                                                                                                                                                                                                                                                                                                                                  cytostatic; tox malignant; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing glioma in brain cell sample involves determining the presence of a nucleic acid encoding an epidermal growth factor receptor mutant protein type {\tt II} -
                                                                                                                                                            07-JUN-1995;
                                                                                                                                                                                                                     US5985553-A
                                                                                                                                                                                                                                                                                                                                                               Human: v-erbB; MAC117; epidermal growth factor receptor; anticancer; cytostatic; toxin; cancer; treatment; detection; mammary carcinoma;
            WPI; 2000-012777/01
                                           Aaronson SA,
                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                         16-NOV-1999
                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           Human EGF receptor DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ23954 standard; DNA; 5532 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 11A-F; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB19259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 gcgagtcgggct 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 gcgagtcgggct 72
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                                          Kraus MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                  91US-0786598.
86US-0836414.
                                                                                                                              87US-0110791
                                                                                                                                                            95US-0475035
                                                                                                                                                                                                                                                                                                                                                  receptor;
                                                                                                                                                                                                                                                /product= "EGF receptor"
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                          King CR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72; DB 21;
Pred. No. 7.1e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ43814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel purified nucleic acid (I) (v-erbB related gene) specifically hybridizing to all or part of a MAC117 gene and not hybridizing to nucleic acid encoding an epidermal growth factor receptor. The product of the invention has anticancer and cytostatic activity. Antibodies to the protein encoded by (I) are conjugated to toxins and kill cancer cells expressing (I). Antibodies to the protein encoded by (I) are useful for the treatment of cancer. Fragments of (I) and the MAC117 gene are useful as probes for the detection of human mammary carcinoma or other malignancies resulting from the v-erbB related gene. This sequence encodes a human epidermal growth factor (EGF)
                                        WPI; 1993-196297/24.
P-PSDB; AAR38211.
                                                                                                                                                                                                                                                                                                                                                                          Epidermal growth factor receptor truncate protein; EGF; binding sites; adsorptive agents; mammalian cell growth abnormality; detection; growth; reproduction; signal transmission; ds.
                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ43814 standard;
            New epidermal growth factor receptor truncate proteins - which
                                                                                                                                            12-JUN-1990;
26-OCT-1990;
                                                                                                                                                                                      12-JUN-1990;
                                                                                                                                                                                                                    08-JUN-1993
                                                                                                                                                                                                                                              US5218090-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     pRLD3D4 construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ43814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5532 BP; 1472 A; 1484 C; 1337 G; 1239 T; 0 other;
                                                                                                              (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 19-30; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purified nucleic acid useful for detection and treatment of mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAY50616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 atgcgaccctccgggacggccggggcagcgctcctggcgctgctgctgcgctctgcccg 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 gcgagtcgggct 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 atgogaccotcogggacggccggggcagegctcctggcgctgctgctgctgctgcccg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcgagtcgggct 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
11 Similarity 100.0%;
72; Conservation
                                                                                                                                            90US-0536896.
90US-0604728.
                                                                                                                                                                                      90US-0536896.
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1077..1079
                                                                                                                                                                                                                                                                            /note= "codon ARA encodes Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 5750 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 5532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of the pRID3D4 construct which encodes the cc epidermal growth factor (EGF) receptor truncate protein LD3D4 (c epidermal growth factor (EGF) receptor truncate protein LD3D4 (c) without transmitting a signal for the growth and reproduction of a cell. It can be used as an adsorptive agent for any moieties that bind the EGF (c) receptor as the portal of entry to a cell. It competes with the EGF (c) receptor present on the cell surface for the binding of ligands and (c) thereby inhibits the action of the ligands or prevents the entry of (c) viruses into cells. It can also be used as for the EGF receptor itself, (c) such as in the detection of abnormalities in mammalian cell growth. (c) It is also useful for preps. novel receptors for efficient detection of ligands and their anti-agonists or agonists. The features table indicate a discrepancy between the LD3D4 protein sequence given (c) in the specification and that which the pRLD3D4 DNA sequence
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 72; Conserv
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                                                                                                                                                                                                                                                                                                                                       binding sites; adsorptive agents; mammalian cell grow detection; growth; reproduction; signal transmission;
                                                                                                                                                                                                                                                                                                                                                      Epidermal growth factor receptor truncate protein; EGF; binding sites; adsorptive agents; mammalian cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ43813;
                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                   PRLD2D3D4
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                                         12-JUN-1990;
26-OCT-1990;
                                                                                                                   08-JUN-1993
                                                                                                                                               US5218090-A
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             (WARN ) WARNER LAMBERT CO
                                                                                      12-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                    construct
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                                           90US-0536896
90US-0604728
                                                                                       90US-0536896
                                                                                                                                                                                                                                                                 Location/Qualifiers 665..2193
                                                                                                                                                                                                      /*tag= a
/codon= 707-708 CG encodes Ile
/note= "encodes LD2D3D4"
1519..1521
                                                                                                                                                                                         /*tag=
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                                                                                                                                                                            "codon ARA encodes Ile"
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Pred. No. 7e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5750;
                                                                                                                                                                                                                                                                                                                                                       growth abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT
AAQ43812
ID AAQ4
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망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of the pRLD2D3D4 construct which encodes the CC epidermal growth factor (EGF) receptor truncate protein LD2D3D4 construct which encodes the protein get binding sites. The protein binds ligands of the EGF receptor cc without transmitting a signal for the growth and reproduction of a cell. It can be used as an adsorptive agent for any molecles that bind the EGF cc receptor as the portal of entry to a cell. It competes with the EGF cc thereby inhibits the action of the ligands or prevents the entry of cc thereby inhibits the action of the ligands or prevents the entry of cc such as in the detection of abnormalities in mammalian cell growth. It is also useful for preps. novel receptors for efficient detection co fligands and their anti-agonists or agonists. The features table cc indicates the discrepancies between the LD2D3D4 protein sequence given in the specification and that which the pRLD2D3D4 DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New epidermal growth factor receptor truncate proteins - which bind ligands of EGF receptor without transmitting signal for growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-196297/24.
P-PSDB; AAR38210.
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                                                                                                                                                                                                                                                                       Epidermal growth factor receptor truncate protein; EGF; growth; binding sites; adsorptive agents; mammalian cell growth abnormality; detection; reproduction; signal transmission; pRLD1D2D3ApaL; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ43812 standard; DNA; 6274 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6207 BP; 1474 A; 1620 C; 1670 G; 1442 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    given in the specification would encode.
                                                                                                                           misc_feature
                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                         pRLD1D2D3.ApaL construct.
                                                                                                                                                                                                                                                                                                                                                                         20-OCT-1993
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                            08-JUN-1993
                                                             US5218090-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    724 gcgagtcgggct 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                           /codon= 707-708 CG encodes Ile
/note= "encodes LD1D2D3ApaL"
1939..1941
                                                                                                                                                                                          Location/Qualifiers 665..2253
                                                                                                                                                                             /*tag=
                                                                                             /note= "codon ARA encodes Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%;
98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60; DB 14;
Pred. No. 6.6e-07;
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12-JUN-1990;

90US-0536896

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC The sequence is that of the pRLDID2D3 construct which encodes the epidermal growth factor (EGF) receptor truncate protein LDID2D3Apal having EGF binding sites. The protein binds ligands of the EGF receptor without transmitting a signal for the growth and reproduction of a cell. It can be used as an adsorptive agent for any moieties that bind the EGF CC receptor as the portal of entry to a cell. It competes with the EGF CC receptor present on the cell surface for the binding of ligands and CC thereby inhibits the action of the ligands or prevents the entry of CC viruses into cells. It can also be used as for the EGF receptor itself, CC such as in the detection of abnormalities in mammalian cell growth. CC of ligands and their anti-agonists or agonists. The features table collidates the discrepancies between the LDID2D3 protein sequence given the specification and that which the pRLDID2D3 DNA sequence
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Best Local !
                                     3 ' UTR
                                                                               CDS
                                                                                                       Key
5'UTR
                                                                                                                                                 Homo sapiens
                                                                                                                                                                          Epidermal growth factor receptor; EGF receptor related protein; EGFR; ERRP; cell proliferation; colon cancer; antitumour; ss.
                                                                                                                                                                                                                                               19-MAR-2001
                                                                                                                                                                                                                EGF receptor related protein (ERRP) encoding cDNA.
                                                                                                                                                                                                                                                                           AAC84211;
                                                                                                                                                                                                                                                                                                     AAC84211 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6274 BP; 1506 A; 1610 C; 1664 G; 1493 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 3; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or reproduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New epidermal growth factor receptor truncate proteins - which bind ligands of EGF receptor without transmitting signal for growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-196297/24
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26-OCT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                       665 atgcgaccctccgggacggccggggcagcgctcctggcgctgc-ggctgcgctctgcccg 723
                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      gcgagtcgggct 72
                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                  /*tag a 228..1664 /*tag b /
/product 1665..1955
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900S-0604728
                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                     CDNA;
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                                                                                                                                                                                                                                                                                                     1958
                                                "ERRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60; DB
Pred. No. 6.5e
0; Mismatches
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                                                                                                                                                                                                                                                                                                     ВP
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. 6.5e-07;
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RESULT 11
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Best Local S
Matches 54
 CDS
                                 CDS
                                                                                                                                                          Streptomyces verticillus
                                                                                                                                                                                          BLM gene cluster; bleomycin gene cluster; polyketide metabolite; bleomycin; bleomycin analogue; holo-carrier protein; thiazolidin
                                                                                                                                                                              thiazoline; bithiazoline; microbial metabolite; sugar; ss.
                                                                                                                                                                                                                       Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.
                                                                                                                                                                                                                                                  31-OCT-2000
                                                                                                                                                                                                                                                                       AAA58471;
                                                                                                                                                                                                                                                                                              AAA58471 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This DNA encodes an epidermal growth factor (EGF) receptor related protein (ERRP). The ERRP is highly homologous to the mouse EGFR and a truncated rat EGFR. The ERRP can be expressed by standard recombinant methodology. The ERRP acts as a EGFR receptor modulator. The ERRP cDN when transfected into colon cancer cell line is useful for inhibiting proliferation of the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-025007/03.
P-PSDB; AAB48033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1958 BP; 514 A; 524 C; 478 G; 442 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 30-31; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel epidermal growth factor receptor related protein and polynucleotide useful for inhibiting proliferation of cancer cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Majumdar A;
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                                                                                                                                                                                                                                                                                                                                                                                                       gcgagtcgggc 71
                                                                                                                                                                                                                                                                                                                                                                                           atgogaccotcagggaccgcgagaaccacactgctggtgctgctgaccgcgctctgcgcg 287
                                                                                                                                                                                                                                                                                                                                                 gcaggtggggc 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                (first entry)
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                               /transl_except=
/note= "ORF 29;
2767..3486
/*tag= c
/note= "ORF
3527..5593
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                                                                             561..2309
                                                                                      /transl_except=
/note= "ORF 30;
                                                                                                                         223..564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VETERANS AFFAIRS
                                                                                                                                   Location/Qualifiers
                                                                  /*tag≖
                                                                                                               *tag=
                                                                                                                                                                                                                                                                                            DNA; 58857
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76.1%;
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Pred. No. 0
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                                           (pos: 1.
encodes
                                                                                      (pos: 1..3, aa: Met) encodes AAB07556"
          encodes AAB07558'
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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0.0071;
                                           ..3, aa: Met)
AAB07557"
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              WO200040704-A1
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/note* "ORF 24;
21010..24666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_except=
/note= "ORF 27;
5806..12294
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/note- "ORF 20;
35818..37302
                                            /transl_except=
/note= "ORF 9; e
57583..58857
                                                                                                                                                    /note-
53018.
                                                                                                       /note=
55821.
                                                                                                                                                                                                                                                                 /note= "ORF 17;
47178..49985
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37299..39215
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/transl_except=
/note= "ORF 15;
                                                                                                                                                                                                                                                                                        39301..47181
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/note= "ORF 23;
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                                                                                                                              54187
                                                                                                                                                                                /transl_except=
/note= "ORF 14;
                                                                                                                                                                                                                                                                                               /transl_except=
/note= "ORF 18;
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/note= "ORF 19;
                                                                                                                                                                                                                                                                                                                                                                                         /note- "ORF 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2291..15491
                                                                          56090..57586
                                                                                                                                                                 /*tag=
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/note= "ORF 16;
                                                                                /transl_except=
/note= "ORF 10;
                                                                                                                                          /*tag=
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                                                                                                                                     'note=
                                                                                                       - "ORF 11;
L..56093
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*ORF 12;
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                                                                                                                                                           "ORF 13;
                              "ORF 8; encodes AAB07578"
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                                                   = (pos: 1..3, aa: Met)
encodes AAB07577"
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encodes
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encodes
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encodes AAB
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encodes AAB07570"
                                                                                                                                                                                                                                                                         encodes AAB07569"
                                                                                                                                                                                                                                                                                               (pos: 1..3, aa: Met) encodes AAB07568"
                                                                                                                                                                                                                                                                                                                             (pos: 1..3, aa: Met) encodes AAB07567"
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encodes AAB07571"
                                                                                 (pos: 1..3, aa: Met)
encodes AAB07576"
                                                                                                               encodes
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es AAB07572"
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AAB07559*
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AAB07563"
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                                                                                                               AAB07575
                                                                                                                                     AAB07574"
                                                                                                                                                          AAB07573"
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13-JUL-2000

(GEMV ) GENENCOR INT INC

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RRESULT 12
AAV234
XX AAV234
AC AAV234
XX AV234
XX FSeudo
XX Kinase
KW Siqma
XX Siqma
XX WO9806
XX WO9806
XX WO9806
XX WO9806
XX WO9806
XX I16-AUG
XX 16-AUG
XX I6-AUG

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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10786 GGACGGCGGCGCCCCCCCCCCCGCGATGACGGCGGCGAGGCGCTCGTCGGGCTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JAN-1999;
05-FEB-1999;
05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the BLM (Bleomycin) gene cluster, containing open reading frames (ORFs) 8-30. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic domains can be used individually or collectively to produce thiazoline, thiazoline, bithiazoline and bithiazoline-containing microbial metabolites. The BLM gene cluster may also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New bleomycin gene cluster components useful i polyketide metabolites, especially bleomycin, chemically modifying biological molecules -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAB07556, AAB07557, AAB07558, AAB07559, AAB07560, AAB07561, AAB07562, AAB07563, AAB07564, AAB07565, AAB07566, AAB07567, AAB075751, AAB075721, AAB07572, AAB07573, AAB07573, AAB07573, AAB07578, AAB07576, AAB075776, AAB07578.
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                                                                                                                                                                                                                                                                                                       Kinase; LipQ; LipR; lipase expression regulator; DNA binding regulator; sigma 54 promoter; secretion factor; lux-box binding element; orfV-box binding element; regulation cascade; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV23486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV23486 standard;
                                                                                                                                                                                                          WO9806836-A2
                                                                                                                                                                                                                                                       Pseudomonas alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas XcpV secretion
                                                     16-AUG-1996;
                                                                                                       15-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 ggacggccggggcagcgctcctggcgctgctgctggctgcgctctgcccggcgagtcgggc
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99US-0118848.
2000US-0477962.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                     96US-0699092
                                                                                                       97WO-US14450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7256 A;
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Pred.
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RESULT 13
AAA13900/c
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Expression vector for producing heterologous proteins in host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes the XcpV secretion factor of Pseudomonas alcaligenes. The DNA represents a nucleic acid of the invention. The nucleic acids encode: (a) a kinase from a pseudomonad that regulates the expression of a lipase; (b) a DNA binding regulator from a Pseudomonad that regulates the expression of a lipase; (c) a Pseudomonas alcaligenes upstream activating sequence; (d) a P. alcaligenes sigma 54 promoter that regulates the expression of a lipase; (e) a P. alcaligenes secretion factor selected from XcpP, Q, R, S, T, U, V, W, X, Y and Z, and OrfV, X, Y; (f) a P. alcaligenes lux-box binding element; and (g) a orfV-box binding element. The nucleic acids represent parts of a regulation cascade, comprising at its heart a kinase and a DNA binding regulator. These sequences can be used for the production of heterologous proteins in a host cell. The cascade also comprises secretion factors which can
                                                                                           Gerritse G,
                                                                                                                                                                                                                                 11-APR-2000
                                                                                                                                                                                                                                                                   US6048710-A
                                                                                                                                                                                                                                                                                                                                                 Pseudomonas alcaligenes; expression; lipase regulation cascade; kinase; DNA binding regulator; polymerase; promoter; secretion factor; XcpP; XcpQ; XcpR; XcpS; XcpT; XcpU; XcpV; XcpW; XcpX; XcpX; XcpZ; XcpZ; OrfV; OrfX; OrfY; OrfZ; LipO; LipR; upstream activating sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA13900 standard; DNA;
                                         P-PSDB; AAY82597
                                                         WPI; 2000-316896/27.
                                                                                                                                                               16-AUG-1996;
                                                                                                                                                                                               15-AUG-1997;
                                                                                                                                                                                                                                                                                                    Pseudomonas alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas alcaligenes XcpV nucleotide sequence SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding proteins involved in the lipase regulation cascade from P. alcaligenes - useful for controlling production essertion of heterologous proteins in P. alcaligenes
                                                                                                                                                                                                                                                                                                                                    detergent; cleaning formulation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 390 BP; 57 A; 127 C; 154 G; 52 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enhance the secretion of produced proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 37; 106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerritse G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 TGCCACAGCCAGCGCCGCCGGCGTAGCTCTCCTCGCCCTCGCGCGCCCCCGGGCCCCGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 tgcgaccctccgggacggccggggcagcgctcctggcyctgctggctgctgcccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
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                                                                                           Quax WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                             96US-0699092
                                                                                                                                                                                              97US-0911853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28.6;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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RESULT 14
AAT28293
ID AAT282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an expression vector comprising a nucleic acid encoding a kinase and a DNA binding regulator which hybridises under stringent conditions to a nucleic acid isolated from pseudomonas alcaligenes. Also described are: (1) an isolated through the properties of the present of the protein comprising the above expression vector; (2) a method of transforming a host cell comprising adding the above plasmid to host cells under appropriate conditions; (3) a transformed host cell comprising the above expression vector; and (4) a method for producing a protein comprising the steps of obtaining a host cell comprising the above expression vector; and (4) a method for producing a protein, and culturing the host cell under conditions for the expression vector of further comprising nucleic acid encoding the protein, and culturing the host cell under conditions for the expression of protein. The expression vector of the present invention can be used for producing heterologous proteins in host cells, particularly, lipase in Pseudomonas. Lipases produced can be used in detergents and cleaning formulations in Industrial processes. The invention provides a higher production level and efficiently express a heterologous protein. The present sequence encodes XcpV isolated from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                         (JOSL-)
New insulin receptor substrate polypeptide and corresp. nucleic rectors, antibodies etc., useful for diagnosis, treatment and
                                                                                                        Pierce JH,
                                                                                                                                                                                                                                                                                                                                                      CDS
                                                       P-PSDB; AAR96994
                                                                      WPI; 1996-209351/21.
                                                                                                                                                                                             03-OCT-1994;
                                                                                                                                                                                                                               03-OCT-1995;
                                                                                                                                                                                                                                                                 11-APR-1996
                                                                                                                                                                                                                                                                                                  W09610629-A1
                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; vector; antibody; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT28293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT28293 standard; cDNA; 4088 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse IRS-2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprises a nucleic acid encoding a kinase and a DNA binding regulator which hybridizes under stringent conditions to nucleic acid \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRS-2; insulin receptor substrate-2; diabetes; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 TGCCACAGCCAGCGCGCGCGCGTAGCTCTCCTCGCCCTGCTCGCGGCCCTCGCCCGG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 tgcgaccctccgggacggccggggcagcgctcctggcgctgctgctgcgctctgcccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Fig 3; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                       JOSLIN DIABETES CENT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                             94US-0317310.
                                                                                                                                                                                                                             95WO-US13041.
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                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 60..4025
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Pred. No. 44;
                                                                                                                                          SERVICES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
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RESULT 15
AAV23494/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A partial CDNA sequence (AAT28293) codes for mouse insulin receptor substrate-2, or IRS-2 (AAR06994), a substrate for the insulin receptor, interleukin-4 receptor and interleukin-15 receptor. The cDNA clone was isolated from a mouse lung cDNA library by screening with clones from other libraries obtd. using probe 60 (see AAT28294-95). The open reading frame shows 51% identity to the IRS-1 sequence. IRS-2 expression was detected in heart, brain, spleen, lung, liver, skeletal muscle, kidney, testis and FDC-P2 cells. The cDNA can be used for prodn. of recombinant IRS-2 or as a probe e.g. transgene can be used to study insulin-related disorders, e.g. type II diabetes. IRS-2 genes may also be used in gene
                                                                                                                                                                                                                                                                                                                                                               Kinase; LipQ; LipR; lipase expression regulator; DNA binding regulator; sigma 54 promoter; secretion factor; lux-box binding element; orfV-box binding element; regulation cascade; ss.
           CDS
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                                               CDS
                                                                                                                                                                                                                                                                                                                                       Pseudomonas alcaligenes.
                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas Xpc,
                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV23494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV23494 standard; DNA; 17612 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4088 BP; 810 A; 1400 C; 1187 G; 691 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assessing risk of diabetes etc., also for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                             complement (4151..3510)
                                                                                                                                                                                                                                                                                                                                                                                                              OrfY, OrfV, OrfX operon.
                                                                                                                                                                                                                                                                 complement (3513..1564)
         /product= XcpT
13282..13806
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/product= OrfX
                                                                                                                                                                                            1416..7049
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                                                                                                                                                                                                                                                                              /product= OrfY
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                            product Xcps
                                                                     /*tag=
                                                                                                                                                                   'product- OrfV
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                                  /*tag=
                                                                                           product= XcpR
                                                                                                                    0122..11633
                                                                                                                                                         168..9909
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72.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28.6;
Pred. No. 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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This sequence encodes the Orfy, Orfy, Orfx, and Xpc secretion factors of pseudomonas alcaligenes. The DNA represents a nucleic acid of the invention. The nucleic acids encode: (a) a kinase from a Pseudomonad that regulates the expression of a lipase; (b) a DNA binding regulator from a pseudomonad that regulates the expression of a lipase; (c) a Pseudomonas alcaligenes upstream activating sequence; (d) a P. alcaligenes signa 54 promoter that regulates the expression of a lipase; (e) a P. alcaligenes secretion factor selected from Xcpp, Q, R, S, T, U, V, W, X, Y and Z, and Orfv, X, Y; (f) a P. alcaligenes liav-box binding element; and (g) a regulation cascade, comprising at its heart a kinase and a DNA binding regulator. These sequences can be used for the production of heterologous protuins in a host cell. The cascade also comprises secretion factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                         Nucleic acids encoding proteins involved in the lipase regulation cascade from P. alcaligenes - useful for controlling production and secretion of heterologous proteins in P. alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-FEB-1998
Sequence 17612 BP; 2698 A; 6026 C; 6039 G; 2836 T; 13 other;
                                                                                                                                                                                                                                                Disclosure; Page 43-48; 106pp; English.
                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09806836-A2
                            which can enhance the secretion of produced proteins.
                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-159528/14.
                                                                                                                                                                                                                                                                                                                                                                                                            (GEMV ) GENENCOR INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-1996;
                                                                                                                                                                                                                                                                                                                                        AAW99999
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14869..15822
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14189..14872
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15819..16964
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L3803..14192
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Search completed: January 14, Job time: 4318 sec

Db 14050 TGCCACAGCCAGCGCCCGGCGTAGCTCTCCTTCGCCCTGCTCGCCGCCCTCGCCCGG 13992

Query Match Best Local S Matches 40

Local Similarity nes 40; Conserv

Conservative

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39.7**8**; 67.8**8**;

score 28.6; D
Pred. No. 38;
0; Mismatches

DB 19; 19;

Length 17612; Indels

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Gaps

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Result
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                             SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search time 1700.56 Seconds (without alignments) 454.965 Million cell updates/sec
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                 AW170373 xn60e06.x
AI889079 wj70b02.x
AW163375 au94d11.y
AW163378 au91e07.y
AI554567 tn25f08.x
                                                                  AW138053 UI-H-BI1-
AU099322 AU099322
BE327106 hw07b09.x
BF056131 7j88g05.x
BF058287 7k29all.x
                                                                                                                               Description
         A1935313
        tn25f08.x
wg66b11
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ALIGNMENTS

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	29.6	29.6	29.6	29.6	29.6	30	30	30	30.6	30.6	30.6	30.6	30.6	30.8	31.4	32.2	32.6	33	35.4	37.4	40.6	40.6	40.6	40.6	40.6	40.6	40.6	46.4	52.8	54.6	56.8	60.6	72
		41.1																															
	945	515	486	457	407	955	781	371	1156	679	679	607	576	582	728	562	165	654	430	1053	2936	2662	2456	955	906	740	657	301	349	214	340	502	805
	11	ű							10	10	10	11	10	10	10	10	11	10	11	12	12	12	12	11	11	11	10	11	11	11	13	10	10
,	BF316964	4888	BF624156	BF485106	BG605564	BF066019	CNS01FNB	AV434418		BE413373	AL503950	BF255166	BE471264	BE453010	AL552108	BE704513	BF903827	BE362171	BF660321	AK014017	AK004944	AK004883	AK004911	BF533273	BF232802	BI102081	AI787580	99	BF514337	13	Ç	63	40
	BF316964	AZ848888	BF624156	BF485106	BG605564	BF066019	AL142056	AV434418	BE421073	BE413373	AL503950	BF255166	BE471264	BE453010	AL552108	BE704513	BF903827	BE362171	BF660321		AK004944	AK004883	AK004911	BF533273	BF232802	в1102081	A1787580	R35665 yl	BF514337	BF112288	AQ938957	AI263609	AI740805
	601903917	2M0150P06	HVSMEa001	WHE1793_E	WHE2239_D	HV_CEb001	Anopheles	AV434418	HWM005.E0	MCG011.H0	AL503950	HVSMEf000	WHE0286_B	894067E09	AL552108	Sc01_08d0	MR1-MT028	DG1_84_F1	maa29d03.	Mus muscu	Mus muscu	Mus	Mus muscu	602073728	602023406	602887822	u120a11.y	190f01.s1	UI-H-BW1-	7143g09.	NL1-DO11C	qq89g02.	wg24d08.x

## REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT AW138053 FEATURES COMMENT DEFINITION TITLE JOURNAL source Seq prime POLYA=No. Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Tumor Gene Index Unpublished (1997) Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 243) human. Homo sapiens EST NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), primer: M13 /organism="Homo sapiens" /db\_xref="taxon:9606" /db\_xref="taxon:9606" /clone="IMAGE:271332" /clone\_lib="NCI\_CGAP\_Sub3" /clohe\_lib="NCI\_CGAP\_Sub3" /lab\_host="PHIOB (Life Technologies)" /lab\_host="PHIOB (Life Technologies)" /note="Vector; p773D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; The Location/Qualifiers 1. .243 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.

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ACCESSION
VERSION
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                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 300)

Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., 1809ai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S., Canaba, T., Sujama, A. and Sugano, S., Canaba, C., Canaba
Contact: Yutaka Suzuki
                                                                                          Oligo-capping method 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AU099322
AU099322,1 GI:13550451
EST.
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JIAM 3334 337, 3682-3683, 3798-3803 (IMAGE CloneIDS 1322317, 1456008-1456775 150855): NCI_CGAP_Kid5 pool 1

JIAM 338-3342

J150555-1502855); NCI_CGAP_Kid5 pool 1

LIAM 3372-3725, 3776-3778 (IMAGE CloneIDS 1323912-132581, 1471368-1472903, 1492104-1493255); NCI_CGAP_LU5 pool 1

LIAM 3575-3582, 3851-3854 (IMAGE CloneIDS 1414920-1417991, 1520904-1522499); NCI_CGAP_GC4 pool 1

LIAM 3575-3582, 3851-3854 (IMAGE CloneIDS 125706-1258631, 1469064-1470983, 147592-1476743); NCI_CGAP_EDS 1057096-1258631, 1469064-1470983, 1475592-1476743); NCI_CGAP_EDS 2000 1

LIAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 985608-986759, 1101192-1101959, 1217928-1220615); NCI_CGAP_EDS 1057416-1061255, 1144588-1145351). Subtraction was performed as previously described [Bonaldo, Lennon 6 Soares (1996): Normalization and Subtraction: Two Facilitate Gene Discovery Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI_CGAP_Sub3 library is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from B1. B1 constitutes a mixture of 21 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_CO4, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_CO10, NCI_CGAP_CO16, NCI_CGAP_KId5, NCI_CGAP_KId11, NCI_CGAP_LYm2, NCI_CGAP_Br23, NCI_CGAP_KId11, NCI_CGAP_LYm2, NCI_CGAP_Br23, NCI_CGAP_LO16, NCI_CGAP_LU24, NCI_CGAP_LU19, NCI_CGAP_LU24, NCI_CGAP_LU19, NCI_CGAP_LU24, NCI_CGAP_LU19, NCI_CGAP_LU19, NCI_CGAP_LU24, NCI_CGAP_LU19, NCI_CGAP_LU10, NCI_CG
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TAG_TISSUE-lung
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Pred. No. 1.6e-07;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ysuzukieims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                        info@image.llnl.gov
Possible reversed clone: polyT not found
Seq primer: -40Up from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: Ggapbs -[@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
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BE327106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE327106.1 GI:9200882
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/note-*Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LU5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction.
                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3182201"
/clone_lib="NCI_CGAP_Lu24"
                                                                                                                        /tissue_type="carcinoid"
/lab_host="DH10B"
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114 c 99 g 36 t
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Pred. No. 1.6e-07;
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The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo.

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KEYWORDS
SOURCE
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72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 475)
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                                                                                                                                                                                                                   /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3393560"
/clone=lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                           libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares NbHF pool 1: 145032-147385, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HFB-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322833, 326280-32663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento
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                                            Soares and M. Fatima Bonaldo."
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Pred. No. 1.6e-07
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Query Match Best Local Similarity

100.0%;

Score 72; Pred. No.

1.6e-07;

DB 11;

Length 475;

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VERSION
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215 GCGAGTCGGGCT 226
                                                                                                                                155 ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGGCGCTGCTGCGCTCTGCCCG 214
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-rémail.nlh.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael .
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The Soares, Ph.D. CDNA Library Arrayed by: Washington University I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution, NCI-CGAP Clone distribution information can be considered that the constant of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
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72; Conserv
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Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW170373 561 bp mRNA EST 12-NOV-1999 xn60e96.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698114 3' similar to gb:K03193 EPIDERNAL GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN); mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                       Homo sapiens
                                                          EST
                                                                                        (HUMAN);, mRNA sequence. AI858079
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Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organisme"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2698114"
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                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 72; DB 10; 100.0%; Pred. No. 1.6e-07;
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nes 72; Conserv
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                                                                                                                                                                                                                                                                                            AW163375 645 bp mRNA EST 09-NOV-1999 au94d11.yl Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783925 5' similar to 9b:K03193 EPIDERWAL GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN); mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 645)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
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Unsert Length: 1510 Std Brror: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 582)
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//lab_host=*DHIOB (phage-resistant)"
//note=*Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fatima Bonaldo.
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/db_xref="taxon:9606"
/clone="IMAGE:2408139"
/clone_lib="NCI_CGAP_Lu19"
/tlssue_type="squamous cell carcinoma, poorly
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100.0%; Pred. No. 1.6e-07;
htive 0; Mismatches 0;
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 646)
1 (bases 1 to 646)
1 (bases 1, L., Dubuque, T., Geisel, G., Jost, S.,
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
white, Y., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                       AW163038 646 bp mRNA EST 09-NOV-1999 au91e07.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783652 5' similar to gb:K03193 EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN); mRNA sequence.
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Seq primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Other_ESTs: au94d11.x1
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                                                                                                                                                                                                     AW163038.1 GI:6302071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: brain; Vector: pBluescript SK (Stratagene); Site_1: SstI; Site_2: XhOI; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor
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/lab_host="DH10B"
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/clone="IMAGE:2783925"
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Pred. No. 1.6e-07;
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Best Local Similarity
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            Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.

1 (bases 1 to 678)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                 AI554567 678 bp mRNA EST 12-MAY-1999 tn25f08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2166679 3' similar to 9b:K03193 EPIDERWAL GROWTH FACTOR RECEPTOR PRECURSOR
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Contact: Wilson RK
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Unpublished (1997)
                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                (HUMAN);, mRNA sequence.
AI554567
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Location/Qualifiers
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Seq primer: -40RP from Gibco
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This clone is available royalty-free through LLNL; contact the
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Unpublished (1998)
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                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev_stage="5 months post-conception"
/lab_host="DH10B"
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/clone_lib="Schneider fetal brain 00004"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 72; DB 10; Length 646; 100.0%; Pred. No. 1.6e-07;
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                                Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                            Unpublished (1997)
                                                                                                             Tumor Gene Index
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 757)
                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2168679"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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146 ATGCGACCCTCCGGGACGGCCGGGGCAGCGCTCCTGGCGCTGCTGCGCTCTGCCCG 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 atgcgaccctccgggacggcggggcagcgctcctggcgctgctgctgctgcccg 60
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                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1042 Std Error: 0.00
Seq.primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
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www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1220 Std Error: 0.00
Seq primer: -40Up from Gibco
High quality sequence stop: 4466.
                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 798)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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                                                                                                                       quality sequence stop: 468.
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to oligo(dT) primer. Double-stranded with Not I and
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/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                   Location/Qualifiers
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/db_xref="taxon:9606"
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Pred. No. 1.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
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AI740805.1 GI:5109093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                Insert Length: 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                       primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-Morgan: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:2370045"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soares and M. Fatima Bonaldo."
215 c 221 g 167 t
                                                 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
Following HAP purification,
                                                                                                                                                   /clone="IMAGE:2366031"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                /lab_host="DH10B"
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  ibraries were mixed, and ss circles were made in vitro. Ollowing HAP purification, this DNA was used as tracer
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Pred. No. 1.6e-07;
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RESULT COCUS

SOURCE KEYWORDS VERSION

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 502) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI263609 502 bp mRNA EST 03-FEB-1999 902.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clor iMAGE:1938578 3' similar to gb:K03193 EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
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      108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 32208-525895 Soares NbHSP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HF8-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322823, 336280-326663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from
(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
137 c 139 g 117 t l others
                                                                                                       Soares and M. Fatima Bonaldo."
227 c 222 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the same 5 libraries. The pools consisted of the following
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:1938578"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH108"
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Pred. No.
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, 1.6e-07;
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AUTHORS
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SOURCE
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MEDLINE
                                                                                                                                                                                                                    Query Match 78.9%; Score 56.8; DB 13; Length 340; Best Local Similarity 94.5%; Pred. No. 0.00046; Matches 69; Conservative 0; Mismatches 3; Indels 1
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Best Local Similarity 94:0%;
Matches 63; Conservative
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                                                                                                                                                   214 GGCNAGTCGGGCT 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 340)
1 (bases 1 to 340)
2abarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V., Xie,L., Muravenko,O.V., Kozyrev,S., Petrenko,L., Skobeleva,N., Li,J., Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.
Noti clones in the analysis of the human genome
Nucleic Acids Res. 28 (7), 1835-1639 (2000)
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GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: NotI site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Raf.Podowski@cgr.ki.se
                                                                                                                                                                                                                                                                                                                                51 a
                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human NotI clones"
/ 137 c 106 g 42 t
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1. .340
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Pred. No. 6.2e-05;
0; Mismatches 4; Indels 0
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